

# Integrative Genomics Viewer IGV

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  - How to run IGV.
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  - Genome information and annotation.
  - User supplied data.
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  - External data.
- Displaying genomics data
  - Basic visualisation.
  - Data dependent visualisation.

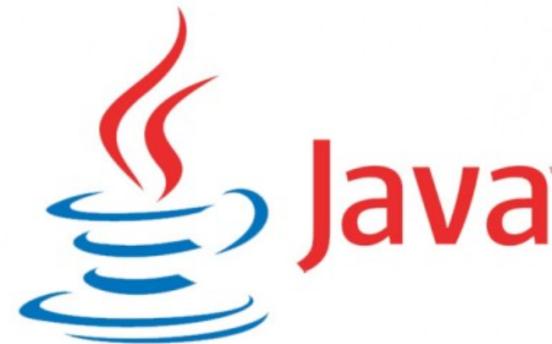
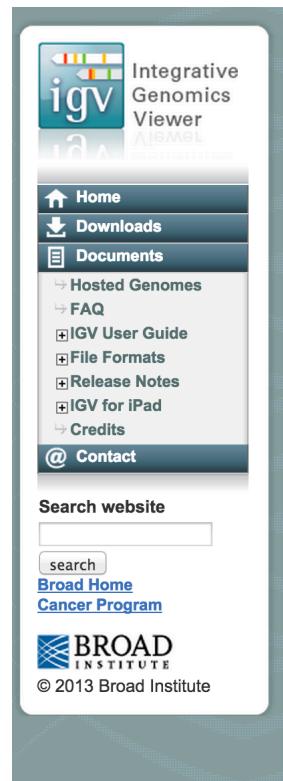
# What is IGV?

- Created by the Broad institute.
- Genome browser.
  - Visualises genomic data (expression, ChIP, resequencing, multiple alignment, shRNA)
  - Handles most common genomic data types.
- Java Desktop application
  - No dependence on server
  - Loads data locally or from URL, consumes memory and CPU.

# How to run IGV?

- Requires Java
- IGV available from Broad

[http://www.broadinstitute.org/  
software/igv/download](http://www.broadinstitute.org/software/igv/download)



Home > Downloads

## Downloads

### Integrative Genomics Viewer (IGV) (Version 2.3)

#### Install IGV

Options for installing and running IGV:

1. (Mac only) Download and run the Mac application; or
2. (All systems) Use the Java Web Start buttons (Mac users: see below for limitations); or
3. (All systems) Download the binary distribution and run IGV from the command line.

#### 1. Mac Application

Download and unzip the Mac App archive, then double-click the IGV application to run it. The application can be moved to the "Applications" folder, or anywhere else. **Note: This requires Java 7. Mac users with Java 6 (JRE 1.6) should use the binary distribution archive or the Java Web Start buttons below.**

[Download Mac App](#)

#### 2. Java Web Start

The buttons below use Java Web Start (JWS) to install and launch IGV directly from our web site.

**\*Mac Users:** The Java Web Start option is not recommended for Mac OSX Mountain Lion or higher. Using it requires that you set Gatekeeper security to its lowest level, and it is possible that even this will not be enough.

**Chrome:** Chrome does not automatically launch the Java Webstart files by default. Instead, the launch buttons below will download a "jnlp" file. This should appear in the lower left corner of the browser. Double-click the downloaded file to run.

- Download to computer.
- Runs locally.
- Archived versions available

### 3. Binary Distribution

Download and unzip the binary distribution archive in a folder of your choosing. IGV is launched from a command prompt -- follow instructions in the "readme" file. To launch igv on Mac or Linux platforms use the shell script "igv.sh". On Windows use "igv.bat".

[Download  
Binary Distribution](#)

#### igvtools

Utilities for preprocessing data files.

- [igvtools 2.3.40.zip](#)

#### Other IGV Versions

[Development Snapshot Build](#) Latest development snapshot; built at least nightly.

[Archived Versions](#)

- Runs from webstart.
- Always runs latest version of IGV.

## 2. Java Web Start

The buttons below use Java Web Start (JWS) to install and launch IGV directly from our web site.

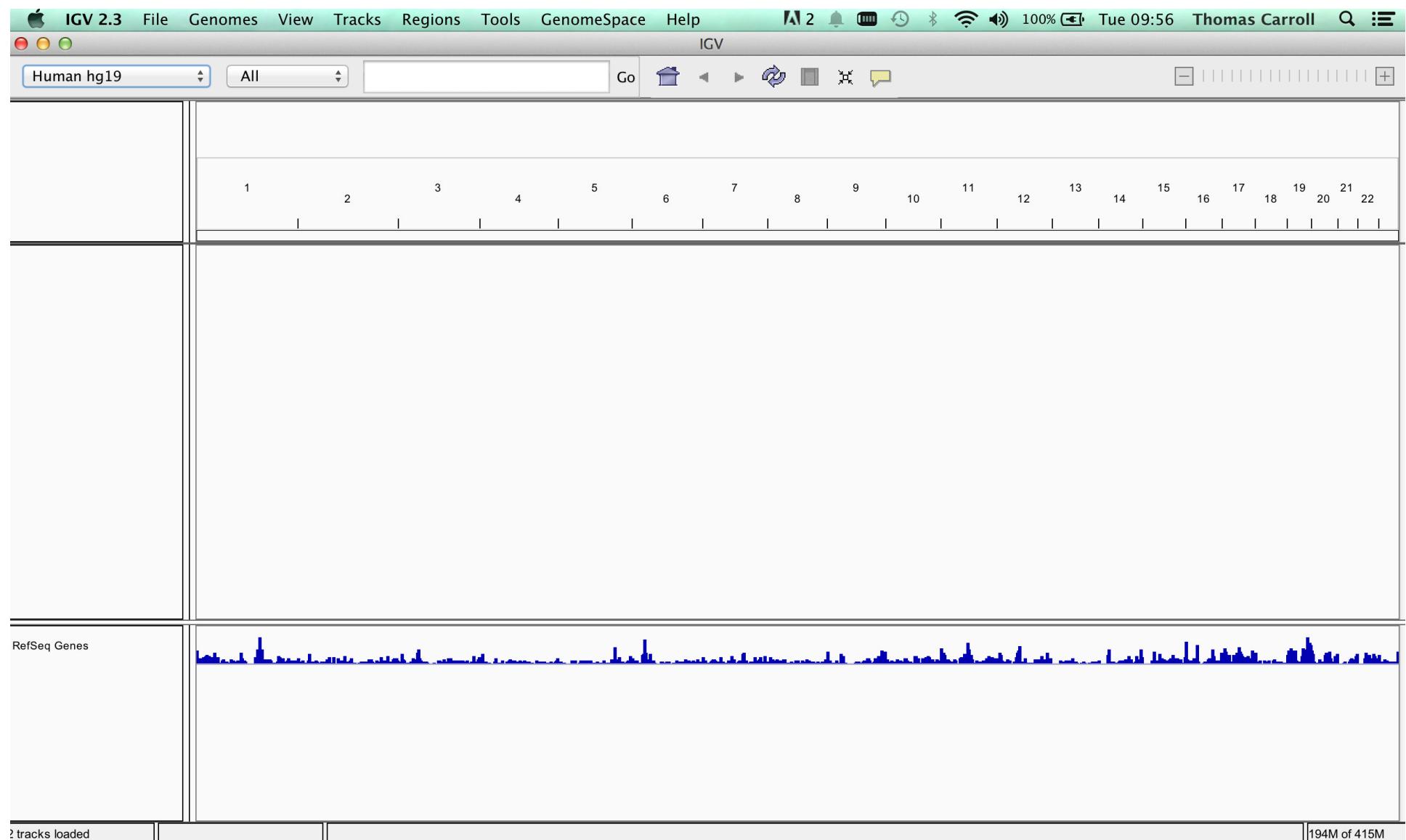
**\*Mac Users:** The Java Web Start option is not recommended for Mac OSX Mountain Lion or higher. Using it requires that you set Gatekeeper security to its lowest level, and it is possible that even this will not be enough.

**Chrome:** Chrome does not automatically launch the Java Webstart files by default. Instead, the launch buttons below will download a "jnlp" file. This should appear in the lower left corner of the browser. Double-click the downloaded file to run.

**Windows users:** To run with more than 1.2 GB of memory you must install 64-bit Java. ***Most Windows installs do not include 64-bit Java by default, even if the operating system is 64-bit.*** Attempting to use the 2GB or greater launch options with 32-bit Java will result in the error "could not create virtual machine".

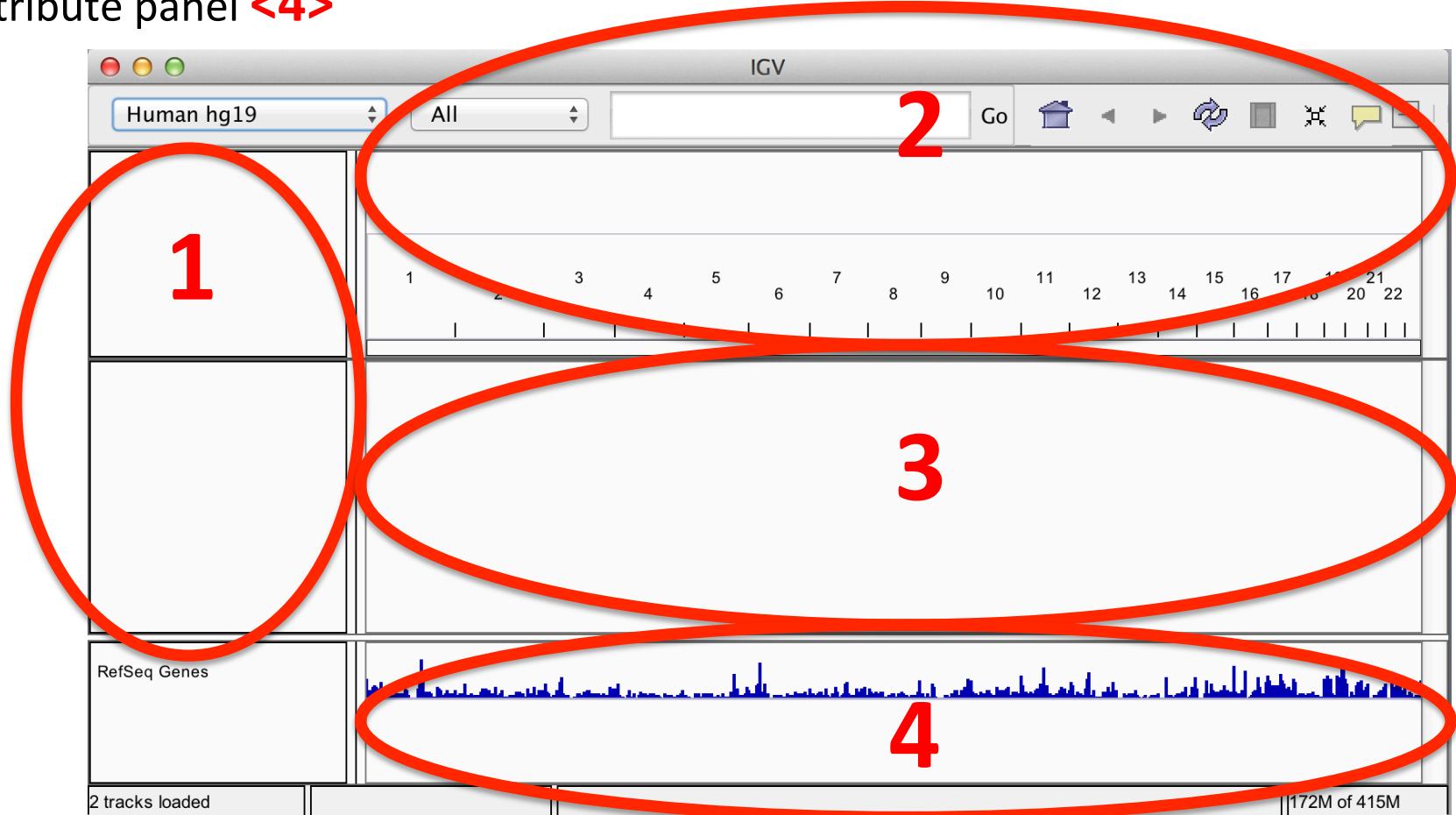
 Launch Launch with 750 MB	 Launch Launch with 1.2 GB  Maximum usable memory for Windows OS with 32-bit Java.	 Launch Launch with 2 GB  Maximum usable memory for 32-bit MacOS.	 Launch Launch with 10 GB  For large memory machines with 64-bit Java.
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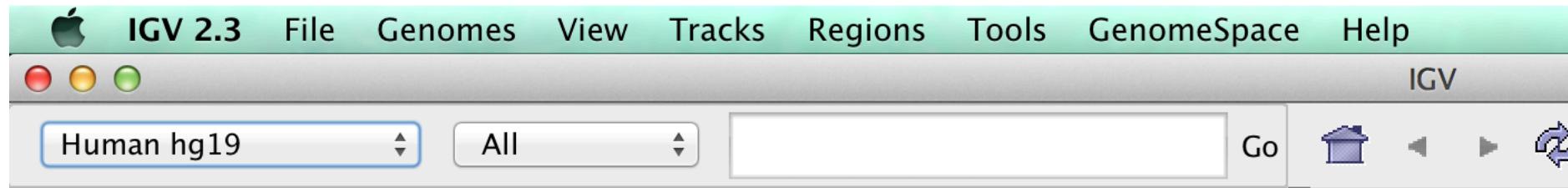
# IGV GUI



- IGV GUI:-

- Sample information panel <1>
- Genome Navigation panel <2>
- Data panel <3>
- Attribute panel <4>

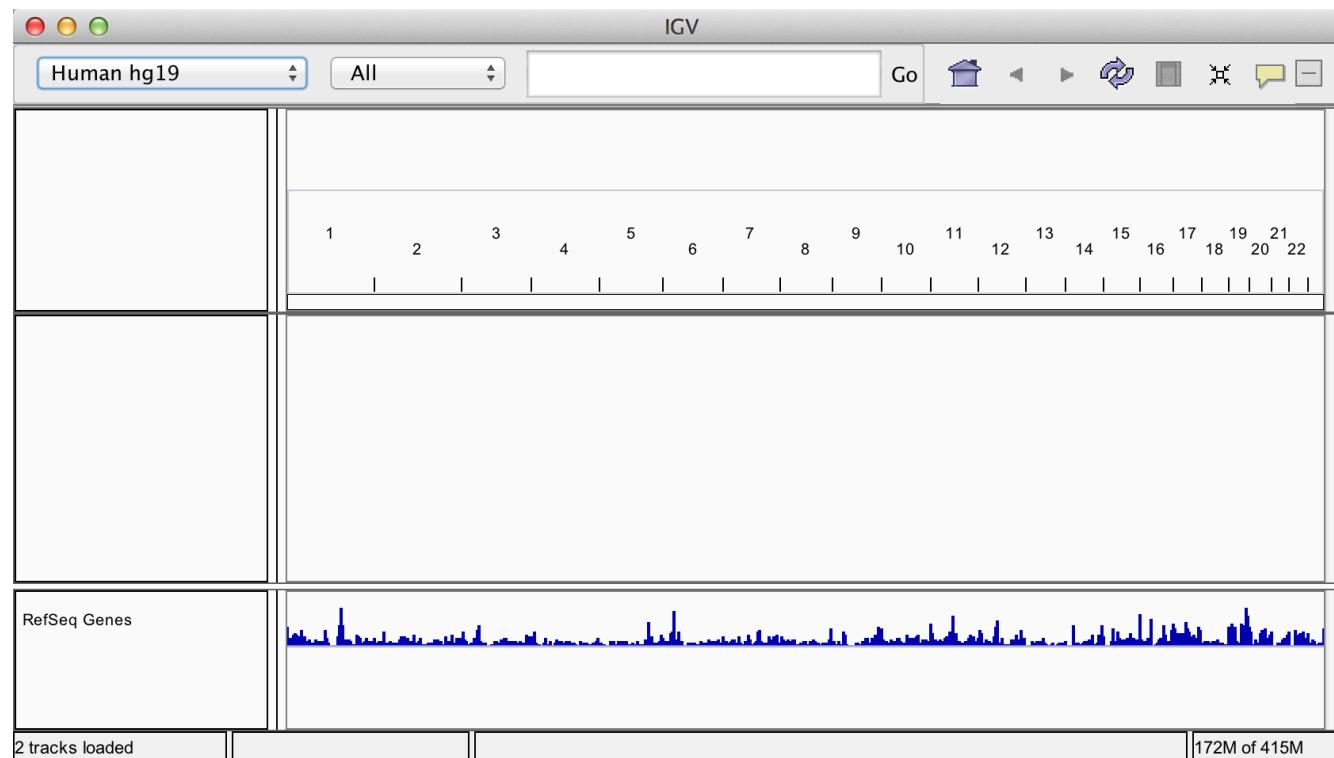




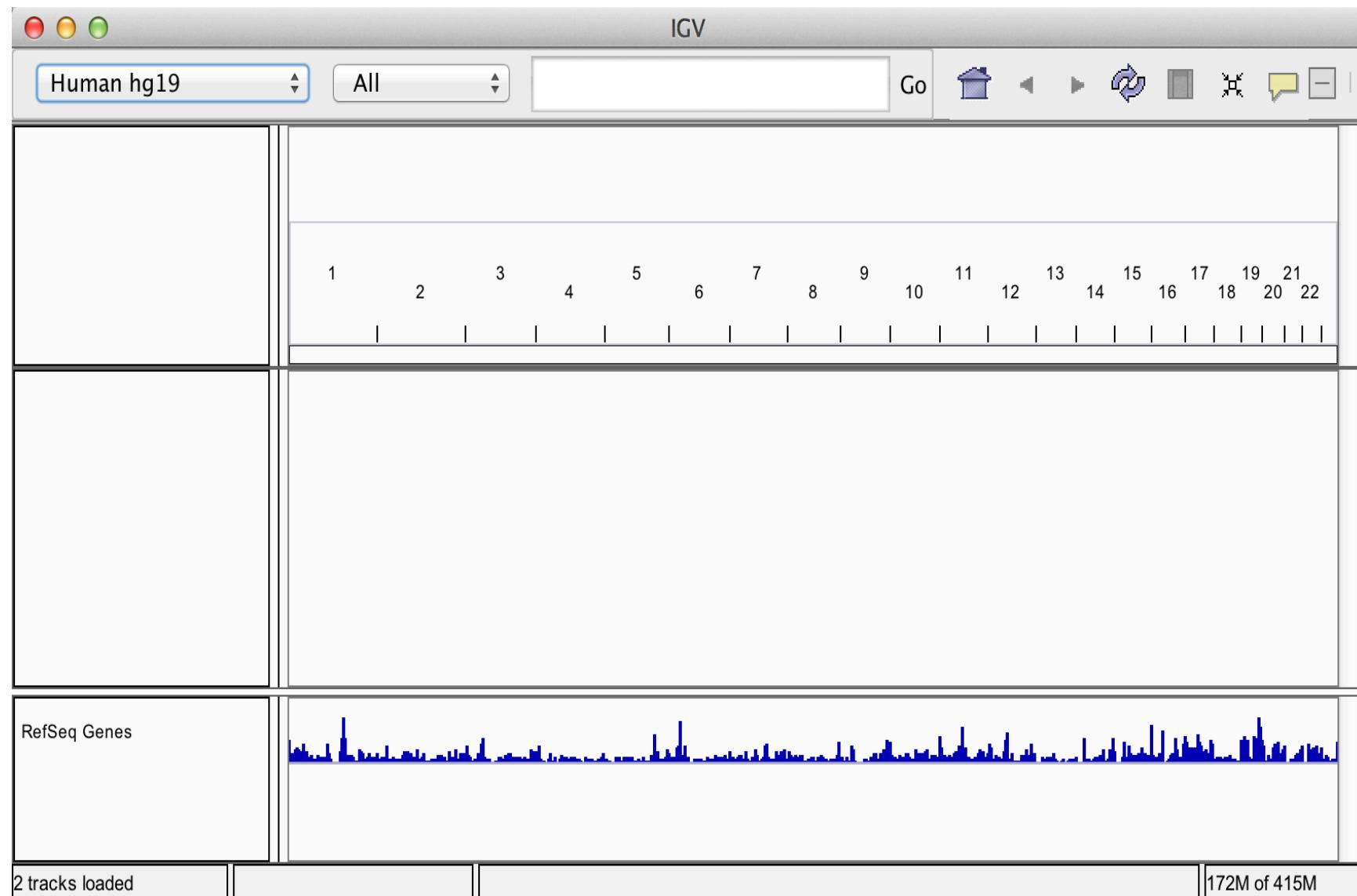
- Menu bar
  - **File**, Load data/sample information.
  - **Genome**, Load and manage genomes.
  - **View**, Display preferences.
  - **Tracks**, Group/sort/filter data tracks.
  - **Regions**, Create region/gene lists.
  - **Tools**, Access to Integrated tools (IGVtools/Bedtools).
  - **GenomeSpace**, Export/import from Genomespace

# Moving around genomes

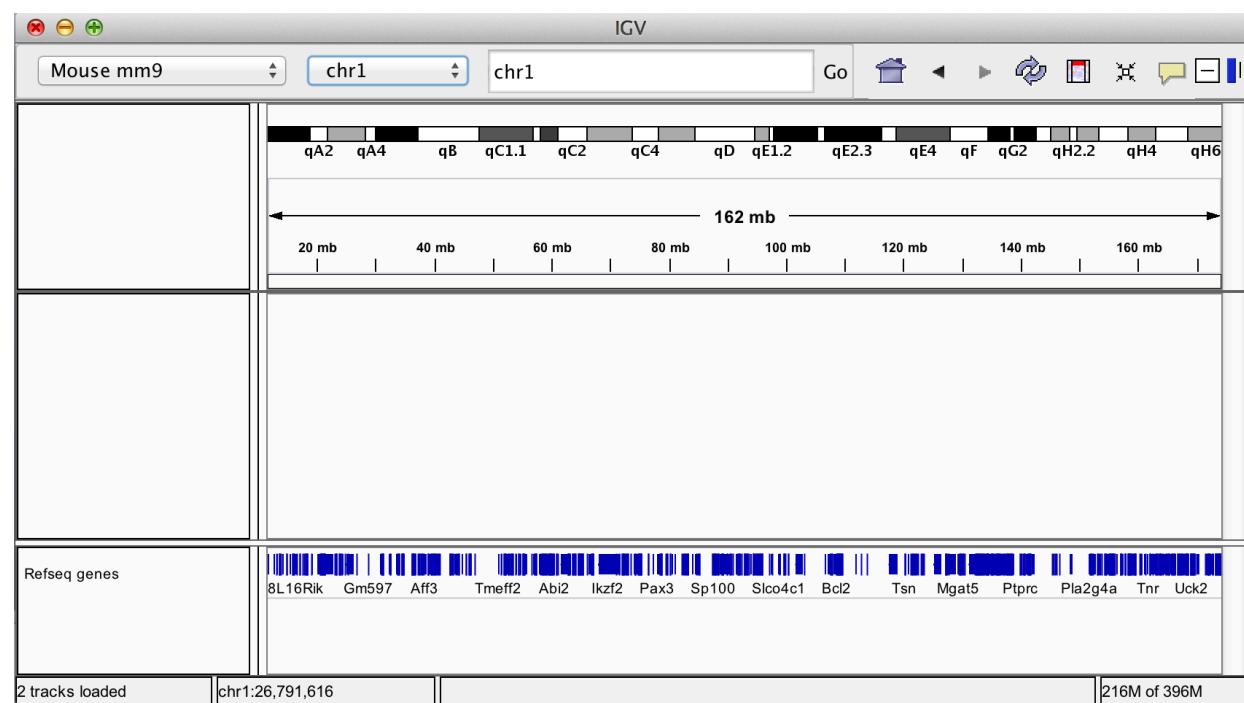
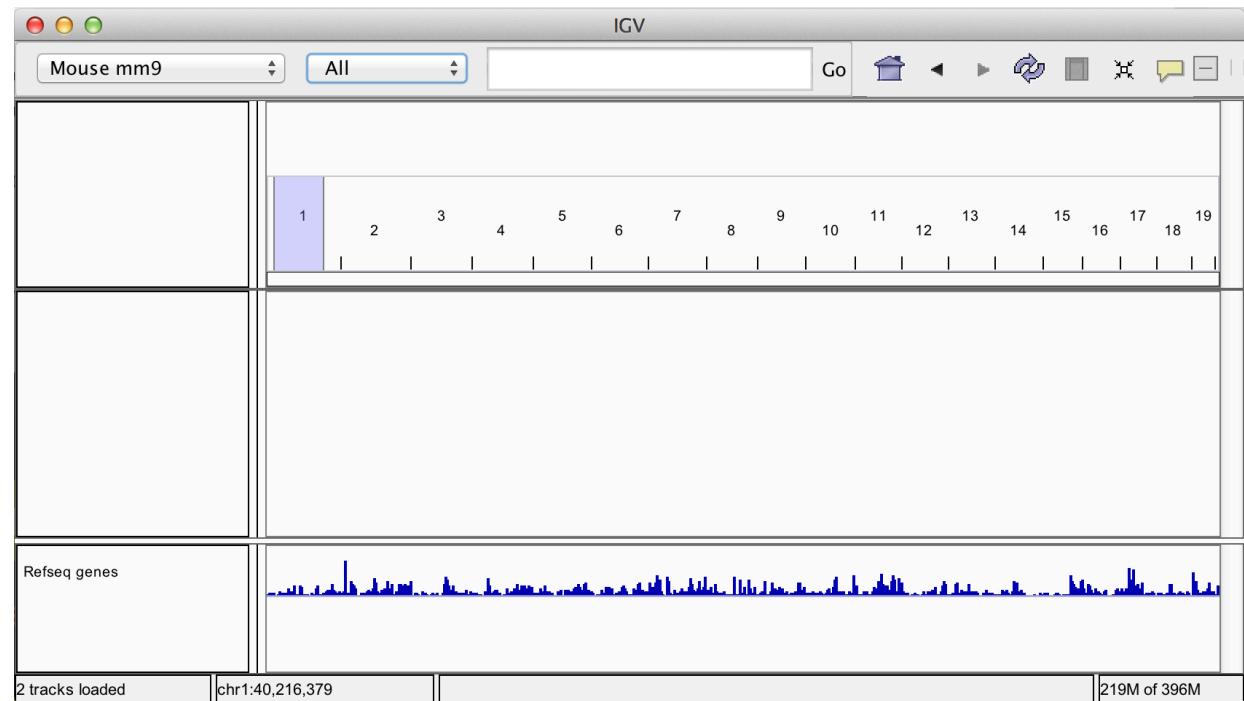
- Cytoband selection and zooming
- Scrolling
- Selection of region of interest



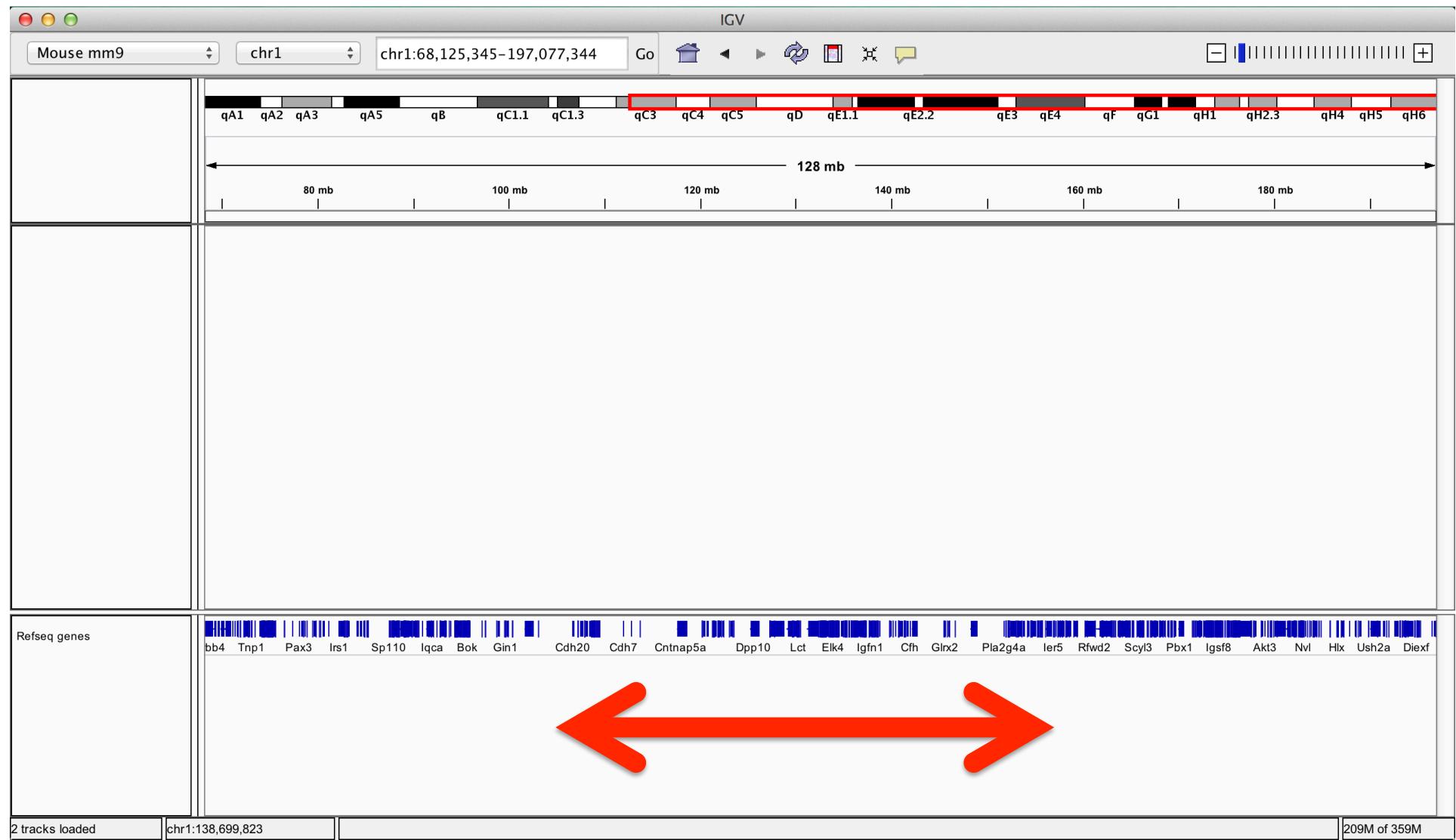
# Whole genome view



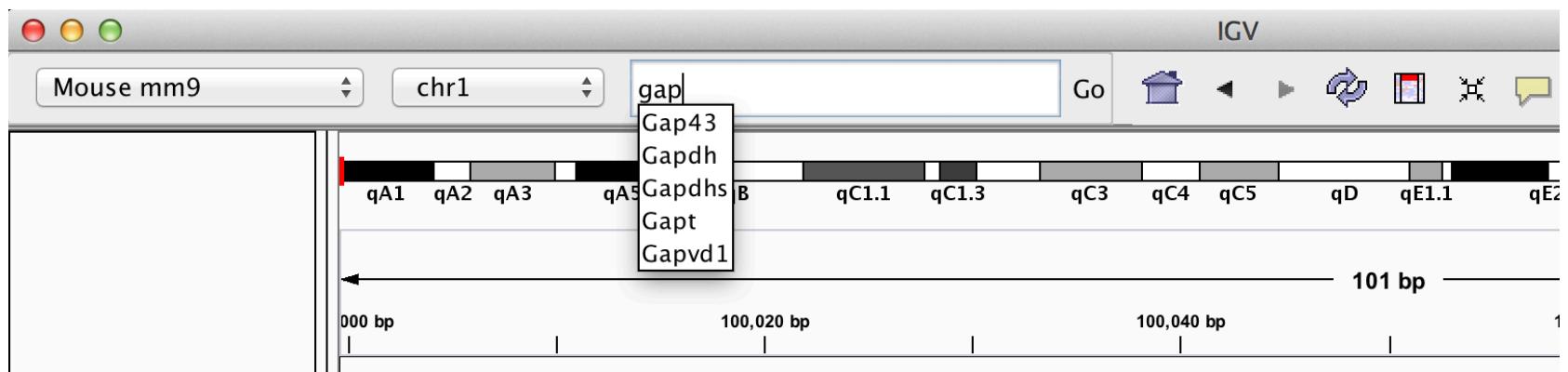
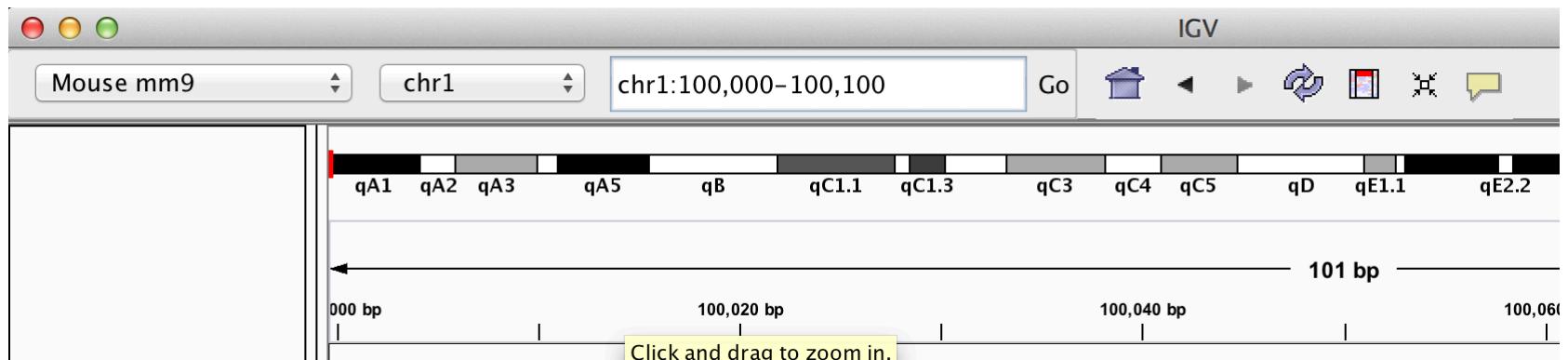
# Zooming



# Scrolling

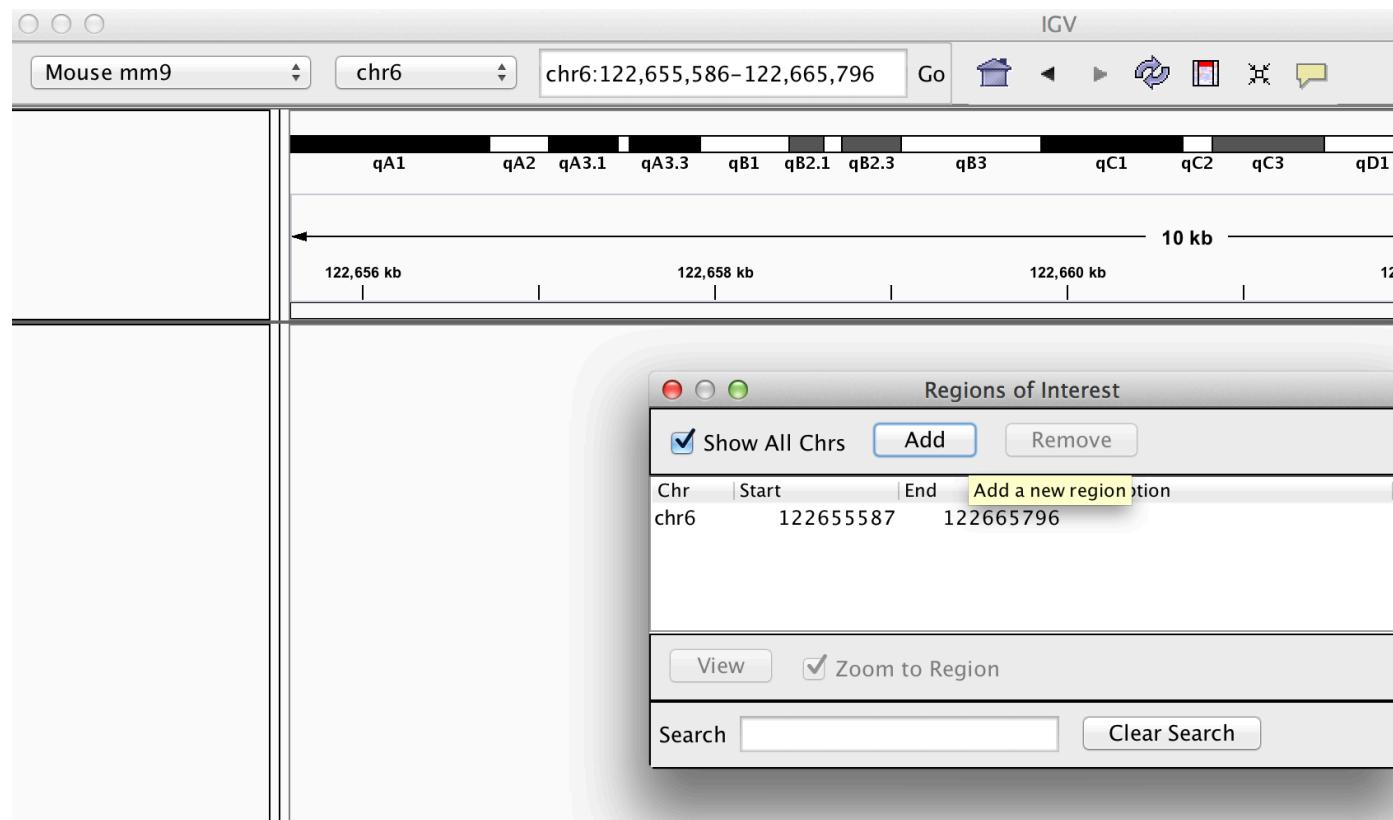
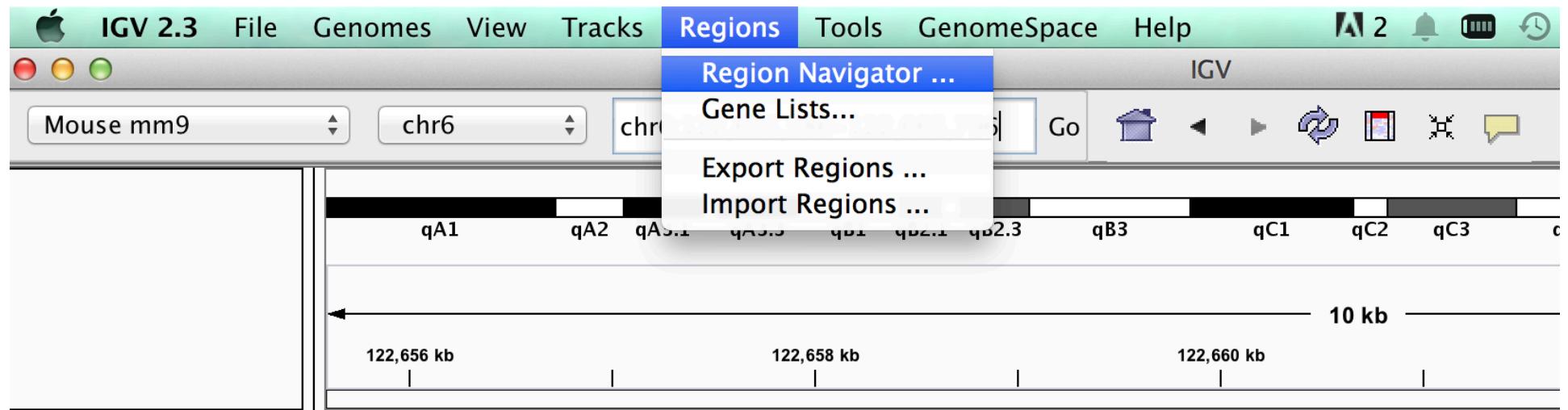


# Jump to Region



# “Bookmarking” regions of interest

- Regions may be added to “Regions of interest”
- These act as bookmarks for areas of particular interest



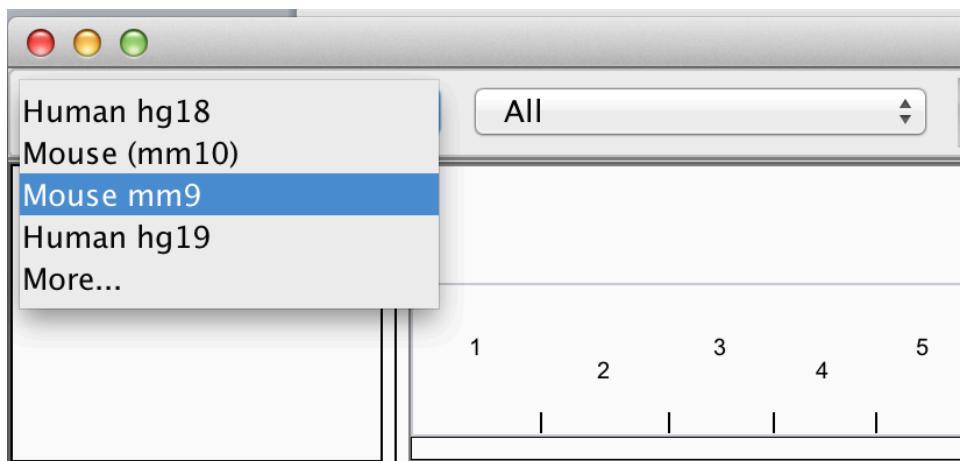
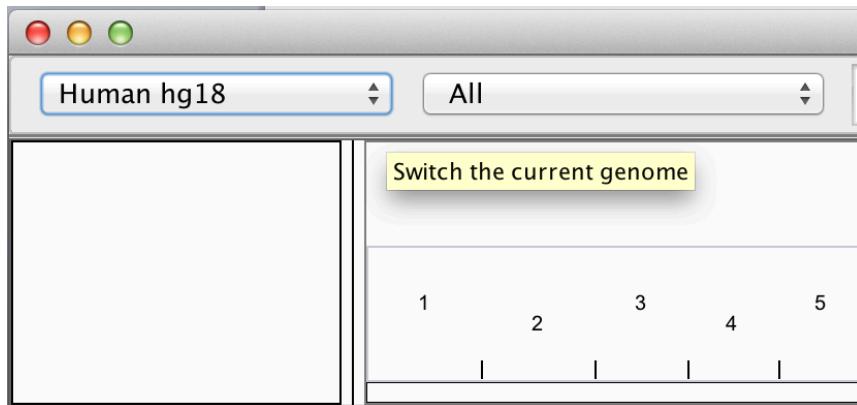
## “Book marked” Region Of Interest



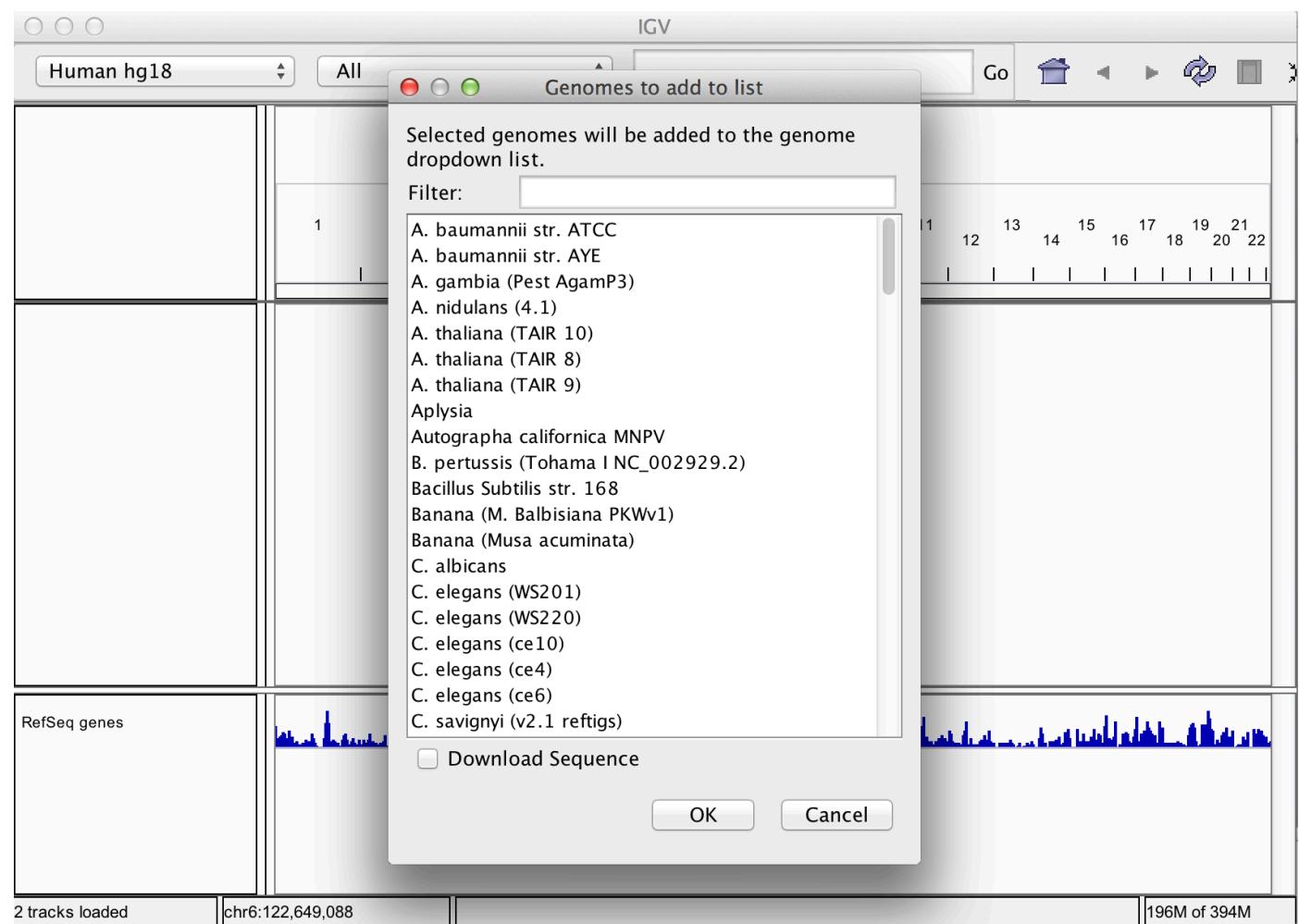
# Loading data in IGV

# Loading Genome Information

- Most genomes can be selected from dropdown.

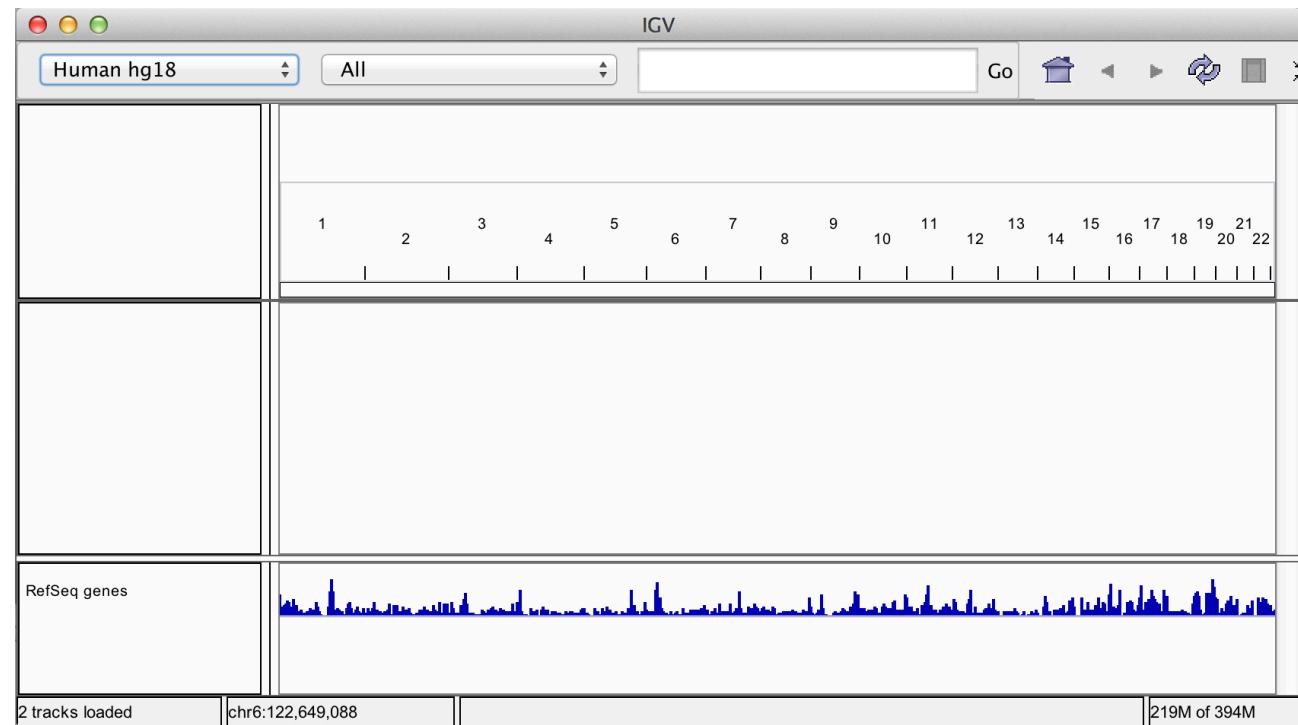


- Genomes not included may be downloaded from repository



# Loading genome annotation

- For supported genomes, gene positions are automatically included in “feature” panel.
- Additional gene positions can be loaded into IGV in gff format.

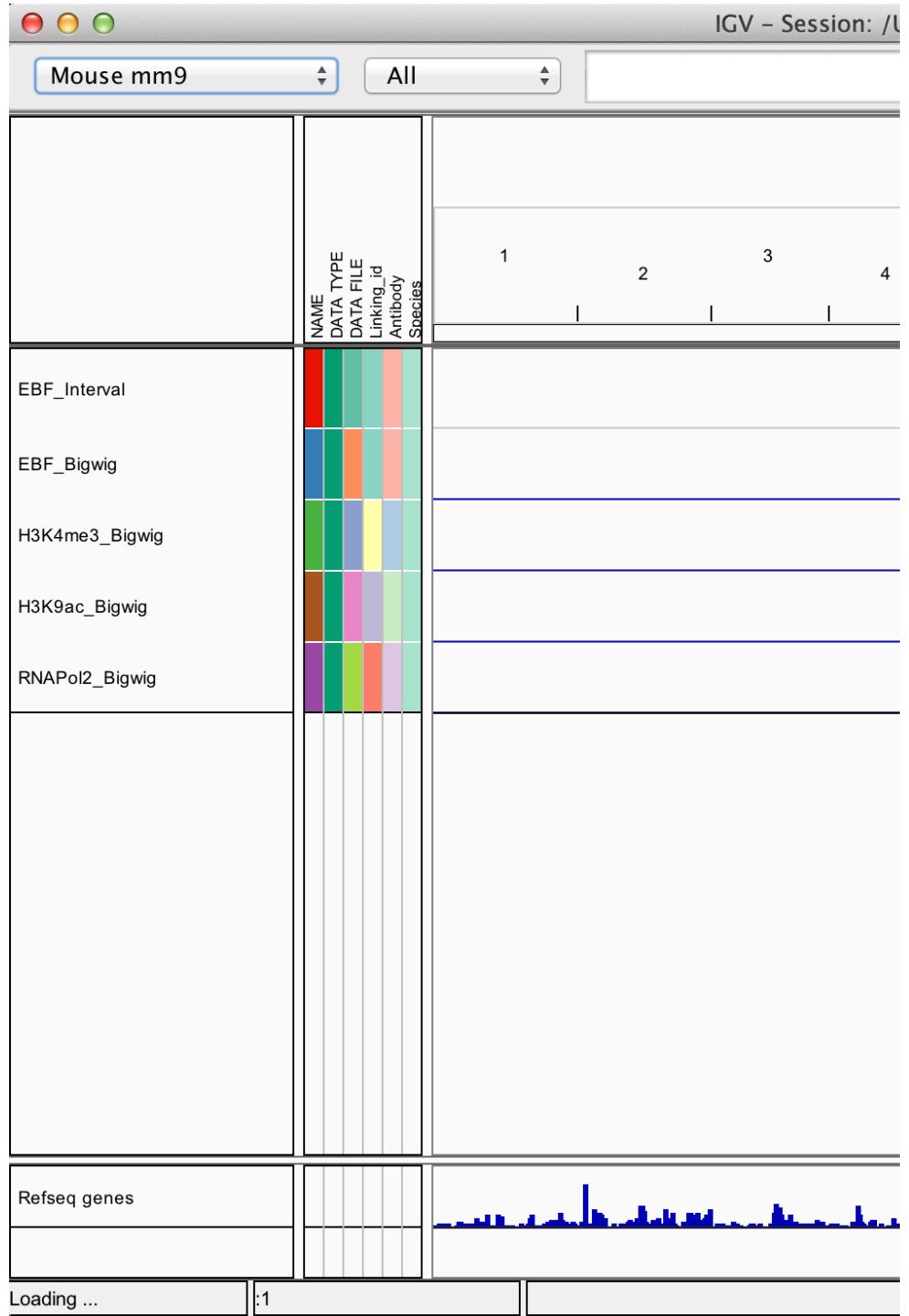


## **Loading sample data.**

- Most common formats can be loaded into IGV through file menu
  - Acceptable data formats include:-
    - BED (.bed)
    - BAM and index (.bam with .bai/.bam.bai)
    - BigWig (.bw)
    - BedGraph/Wig (.bedGraph, .wig)
- And many more...

# Loading sample metadata

- IGV allows the inclusion of information on samples.
- Sample information is then included in sample information panel.



- Example Sample Information file

<http://www.broadinstitute.org/igvdata/exampleFiles/exampleSampleInfo.txt>

TRACK_ID	Data_Type	PARTICIPANT_ID	SAMPLE_ID	GENDER	T/N	Tumor_type	Treated	Primary/Secondary	Hypermutated
EX-01-001	Expression	P-01-P001	P-01-S001	M	Tumor	GBM	Y	Primary	Y
CN-01-002	CopyNumber	P-01-P001	P-01-S001	M	Tumor	GBM	Y	Primary	Y
MU-01-003	Mutation	P-01-P001	P-01-S002	M	Tumor	GBM	Y	Primary	Y
EX-01-004	Expression	P-01-P002	P-01-S003	M	Normal	GBM	Y	Secondary	Y
CN-01-005	CopyNumber	P-01-P002	P-01-S004	M	Tumor	GBM	Y	Secondary	N
EX-01-006	Expression	P-01-P002	P-01-S004	M	Tumor	GBM	Y	Secondary	N
ME-01-007	Methylation	P-01-P002	P-01-S004	M	Tumor	GBM	Y	Secondary	N
EX-01-008	Expression	P-01-P003	P-01-S006	F	Tumor	GBM	N	Primary	Y
EX-01-009	Expression	P-01-P004	P-01-S009	F	Tumor	GBM	N	Primary	Y
EX-01-0010	Expression	P-01-P005	P-01-S0011	M	Control				

# Using sample information.

- Sample information can include discrete and continuous.
- Can be used to “sort” and “filter” tracks.
- Can split tracks across panels by “group”

IGV – Session: /Users/tcarroll/Documents/teste/tracktables/RNAPol

Mouse mm9 All Go

Group By Attribute

Group tracks by:

- None
- NAME**
- DATA TYPE
- DATA FILE
- Linking\_id
- Antibody
- Species

EBF\_Interval

EBF\_Bigwig

H3K4me3\_Bigwig

H3K9ac\_Bigwig

RNAPol2\_Bigwig

IGV – Session: /Users/tcarroll/

Mouse mm9 All Go

Select a chromosome to view

1 2 3 4 5

EBF

H3K4me3

H3K9ac

RNAPol2

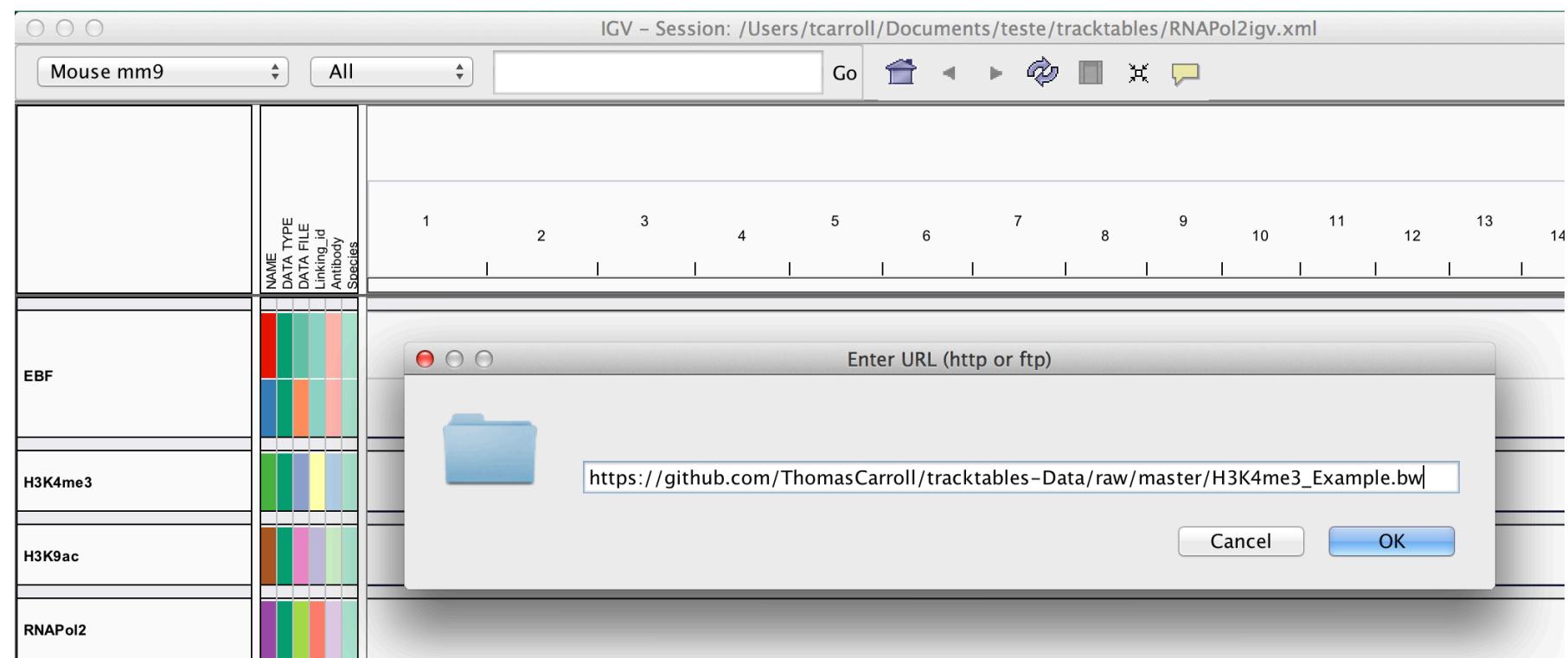
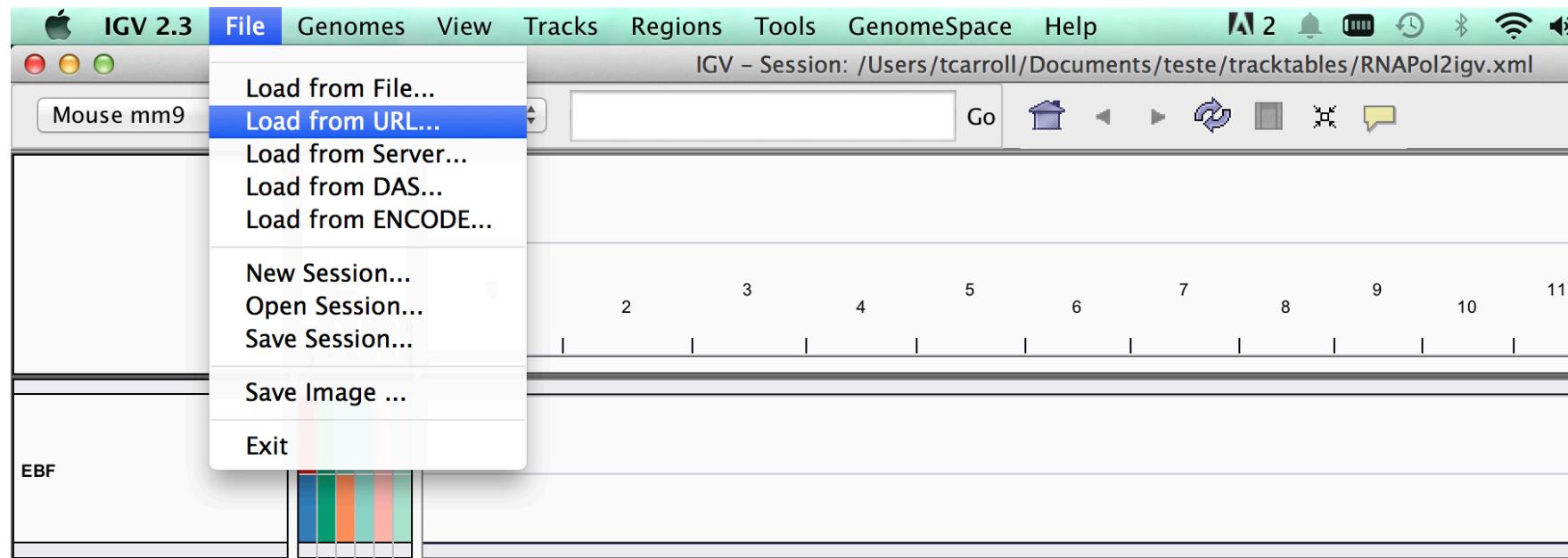
**Grouped related files by name**

**Grouped by unique ID**

# Loading external data and annotation

## **Load data from a URL.**

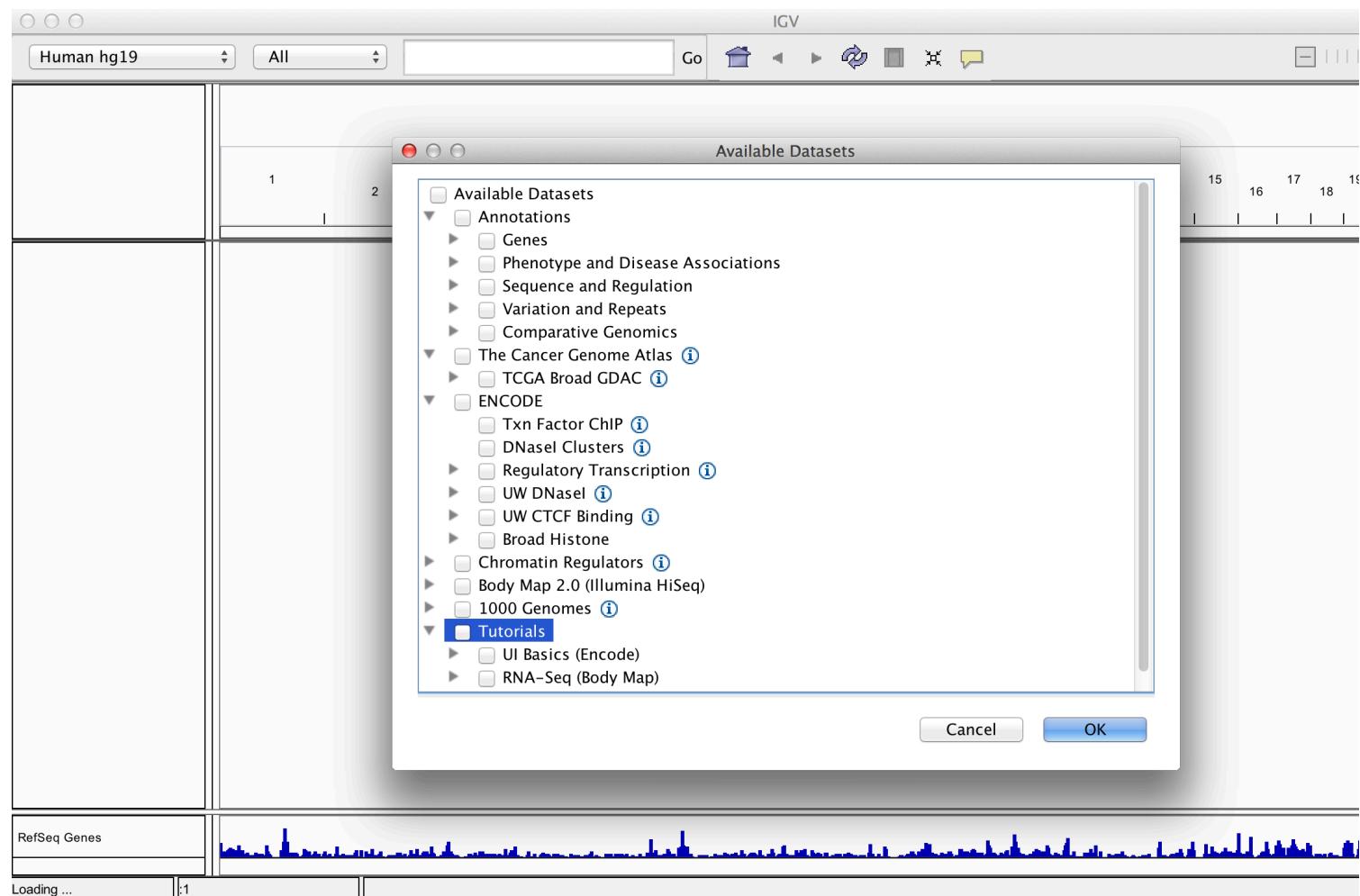
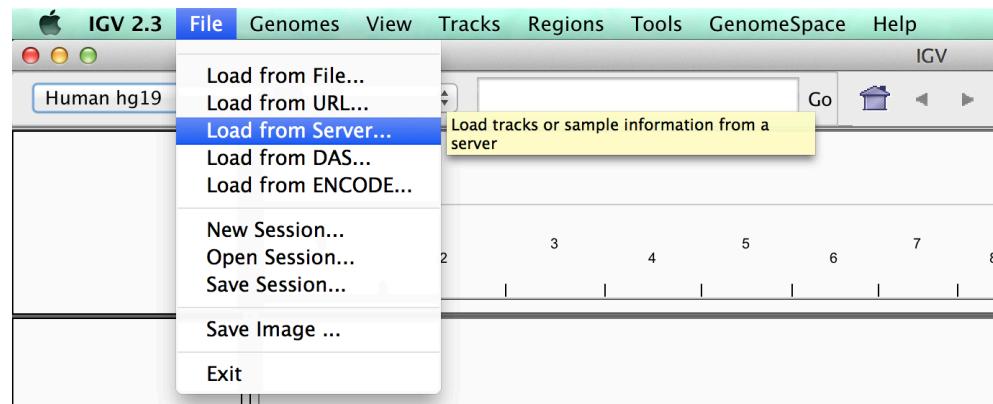
- As with UCSC, IGV supports data hosted on external servers.
- Data accessible from a URL such as HTTP and FTP can be loaded using the **“Load from URL”**.



# Loading external data and annotation

## **Load data from a server.**

- Unlike UCSC, IGV comes with few external tracks.
- External tracks (relevant to the genome) can be loaded from the IGV server or Encode-IGV server.



# Viewing data

- IGV associates common file formats with default display methods.
- Most of the time IGV will make a sensible choice how we wish to display data.

# Accepted formats and default display.

Information on accepted file formats and default display can be found at  
<http://www.broadinstitute.org/software/igv/RecommendedFileFormats>

## Recommended File Formats

The following table lists recommended file formats for data types. **Tip:** Using [igvtools](#) to convert a source data file to a binary TDF file can reduce loading time and improve performance.

Source Data	Recommended File Formats
ChIP-Seq, RNA-Seq	TDF format. Use the <a href="#">igvtools</a> package (count command) to generate a binary read count density file in TDF format. Load the resulting TDF file into IGV.
Copy number	CN format, SNP format  <b>Log values:</b> If copy number data contains negative values, IGV assumes they are scaled log values and displays them without modification. If copy number data contains all positive values, IGV assumes they are unscaled. It centers the unscaled values around 2 (1 for allele specific files), log transforms them ( $\logValue = \log2(copyNumber / 2)$ ), and displays the log values.
Gene expression data	GCT format, RES format

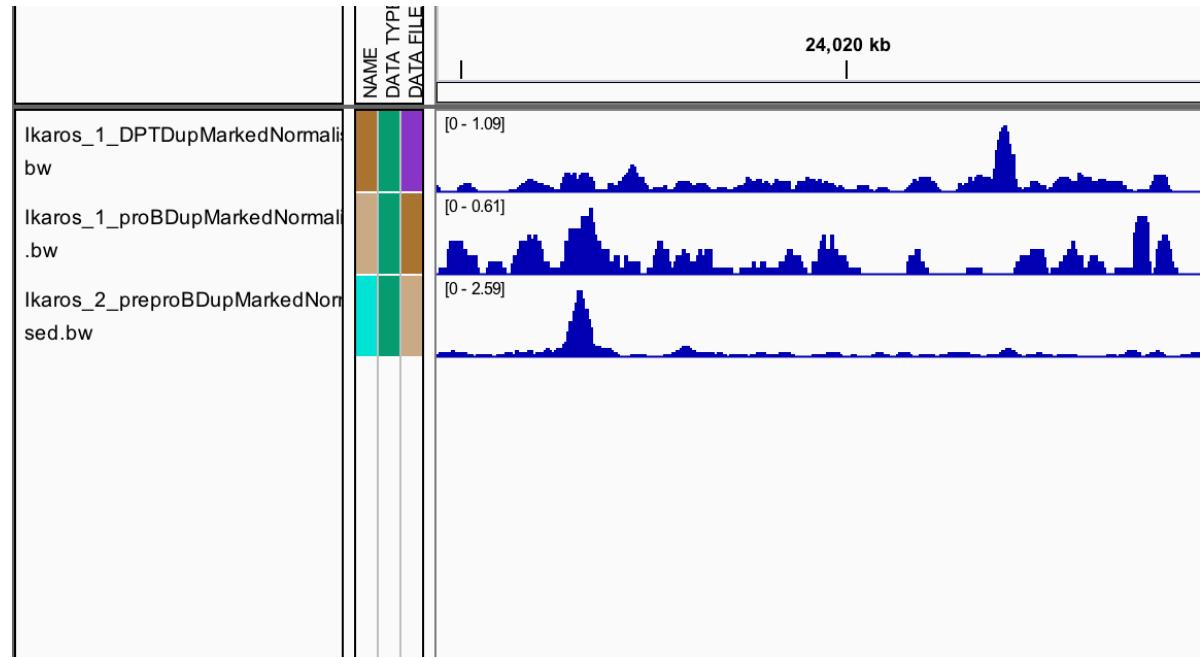
# Bed/bigBed

- Basic
  - Tab-delimited Chrom,Start,End
- Bed6
- bigBed (recommended)



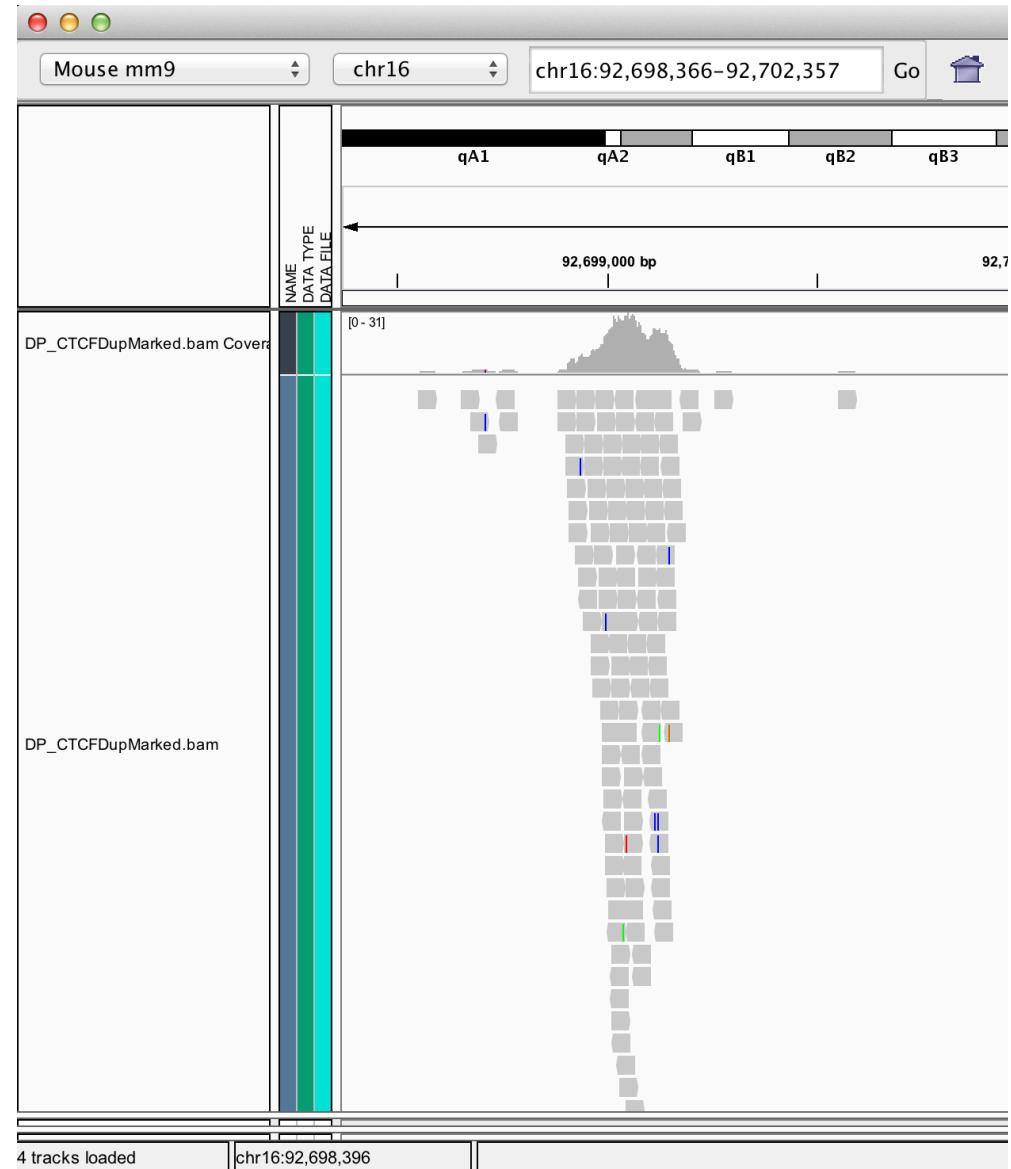
# Wig, BedGraph and BigWig

- Wig/bedGraph require high memory load
- Recommended format is bigWig



# BAM alignment files

- BAM files contain alignment information.
- Require an accompanying .bai index file for display

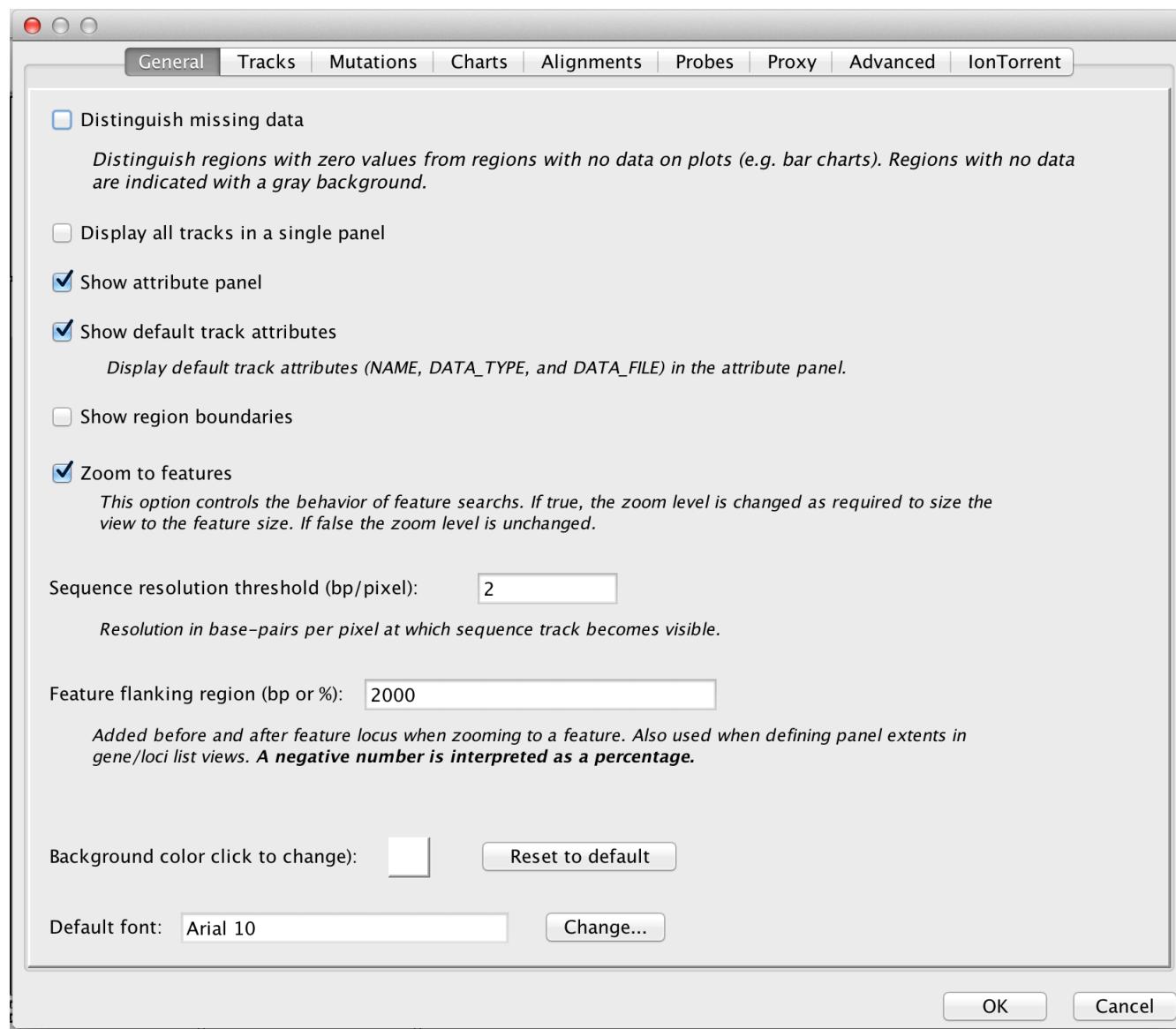


# Finer control of display

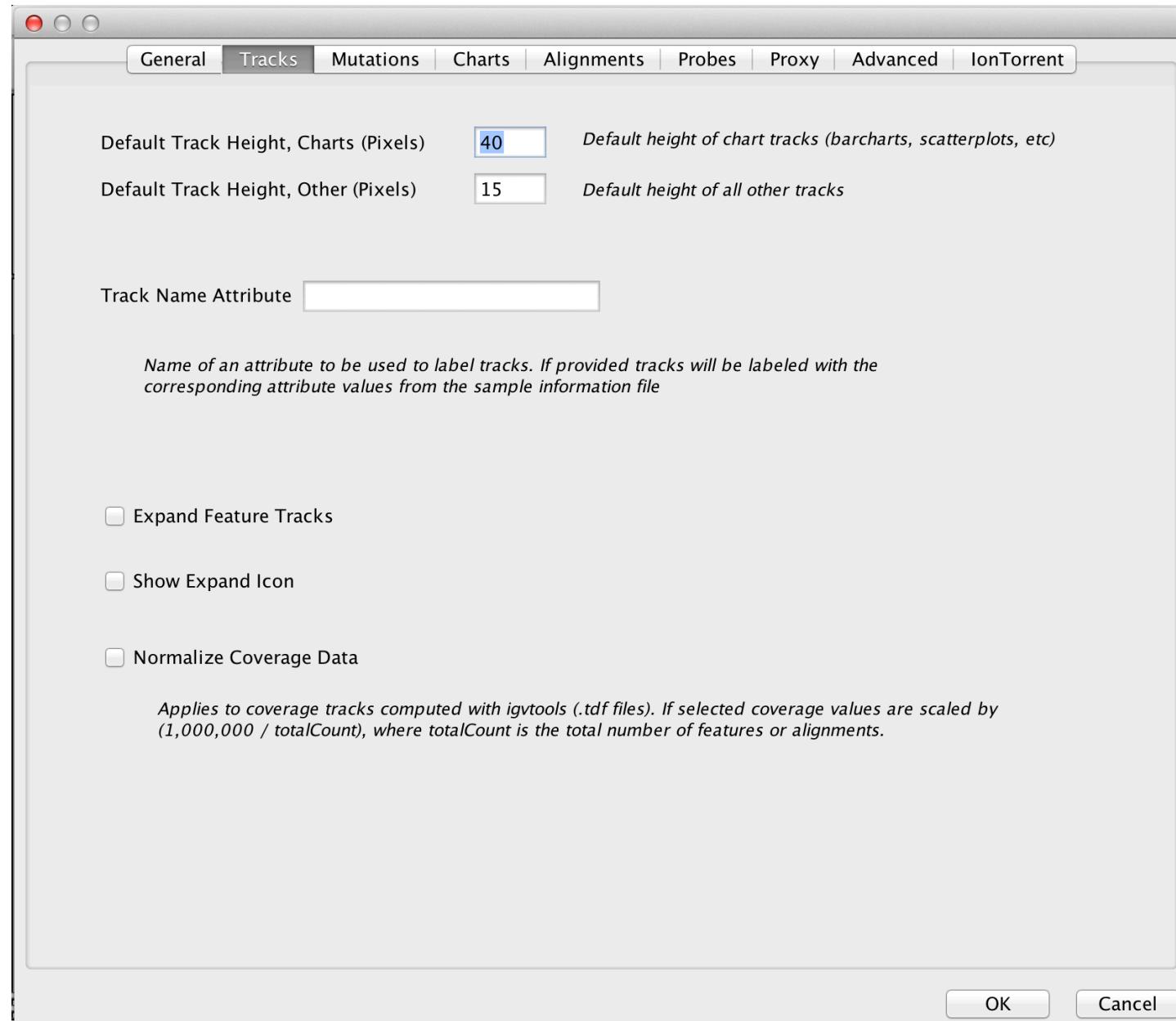
- IGV allows for customization of track display.
  - Menu bar -> View -> Preferences
  - Select track (right click)

# Display preferences

## General



# Tracks



# Alignments

General | Tracks | Mutations | Charts | Alignments **Alignments** | Probes | Proxy | Advanced | IonTorrent

Visibility range threshold (kb):  Nominal window size at which alignments become visible

Downsample reads Max read count:  per window size (bases):

**Filter and shading options**

Coverage allele-freq threshold: <input type="text" value="0.2"/>	Mapping quality threshold: <input type="text" value="0"/>
<input checked="" type="checkbox"/> Filter duplicate reads	<input checked="" type="checkbox"/> Show center line
<input checked="" type="checkbox"/> Filter vendor failed reads	<input checked="" type="checkbox"/> Show coverage track
<input type="checkbox"/> Filter secondary alignments	<input type="checkbox"/> Show soft-clipped bases
<input type="checkbox"/> Filter supplementary alignments	<input type="checkbox"/> Flag unmapped pairs
<input checked="" type="checkbox"/> Shade mismatched bases by quality: <input type="text" value="5"/> to <input type="text" value="20"/>	
<input type="checkbox"/> Flag insertions larger than: <input type="text" value=""/> bases	
<input type="checkbox"/> Filter alignments by read group	URL or path to filter file

**Splice Junction Track Options**

<input type="checkbox"/> Show junction track	Min flanking width: <input type="text" value="0"/>	Min junction coverage: <input type="text" value="1"/>
<input checked="" type="checkbox"/> Show flanking regions		

**Insert Size Options**

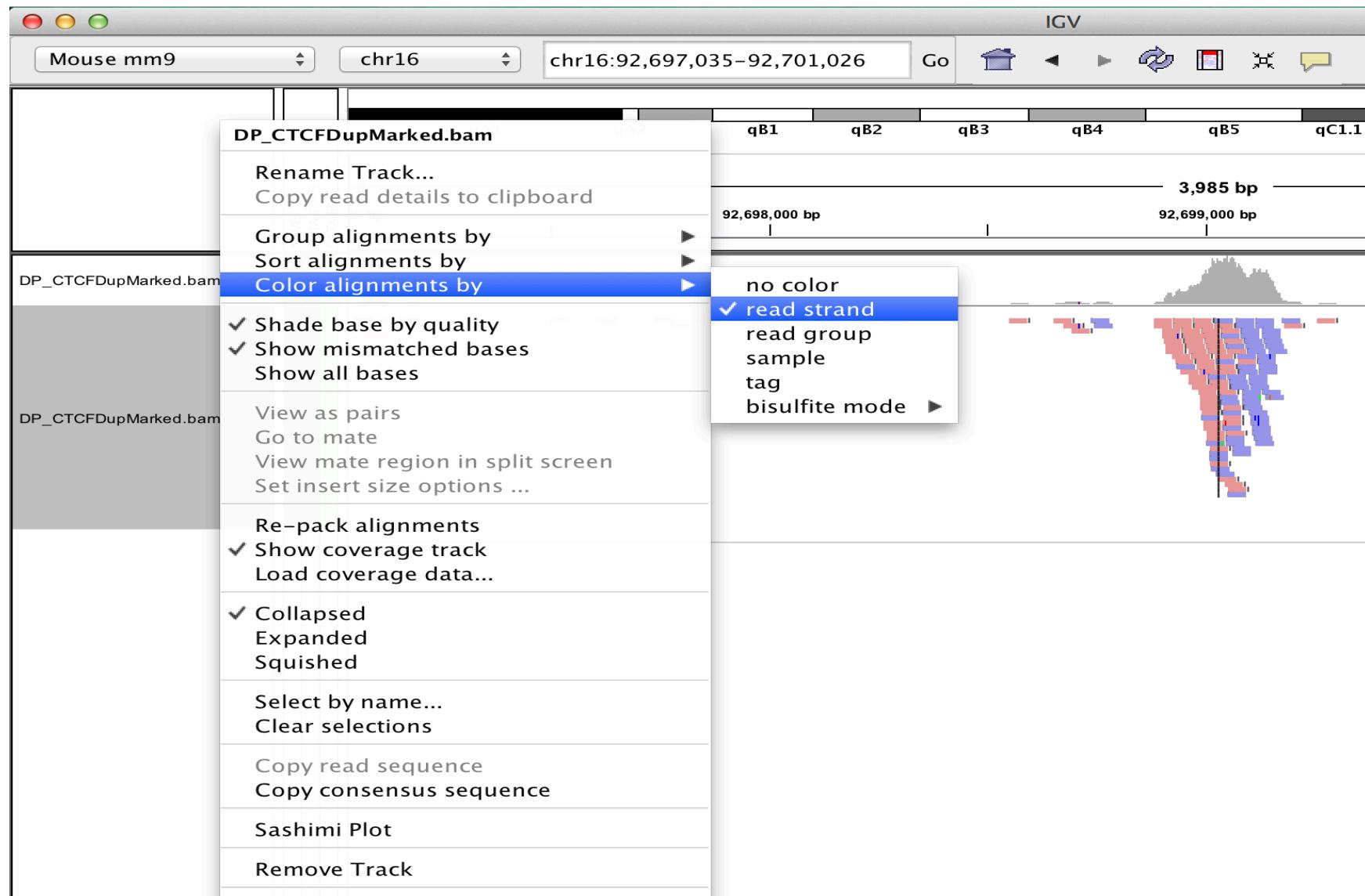
*These options control the color coding of paired alignments by inferred insert size. Base pair values set default values. If "compute" is selected values are computed from the actual size distribution of each library.*

Defaults	Minimum (bp): <input type="text" value="50"/>	<input checked="" type="checkbox"/> Compute	Minimum (percentile): <input type="text" value="0.5"/>
	Maximum (bp): <input type="text" value="1000"/>		Maximum (percentile): <input type="text" value="99.5"/>

OK Cancel

# Track display options

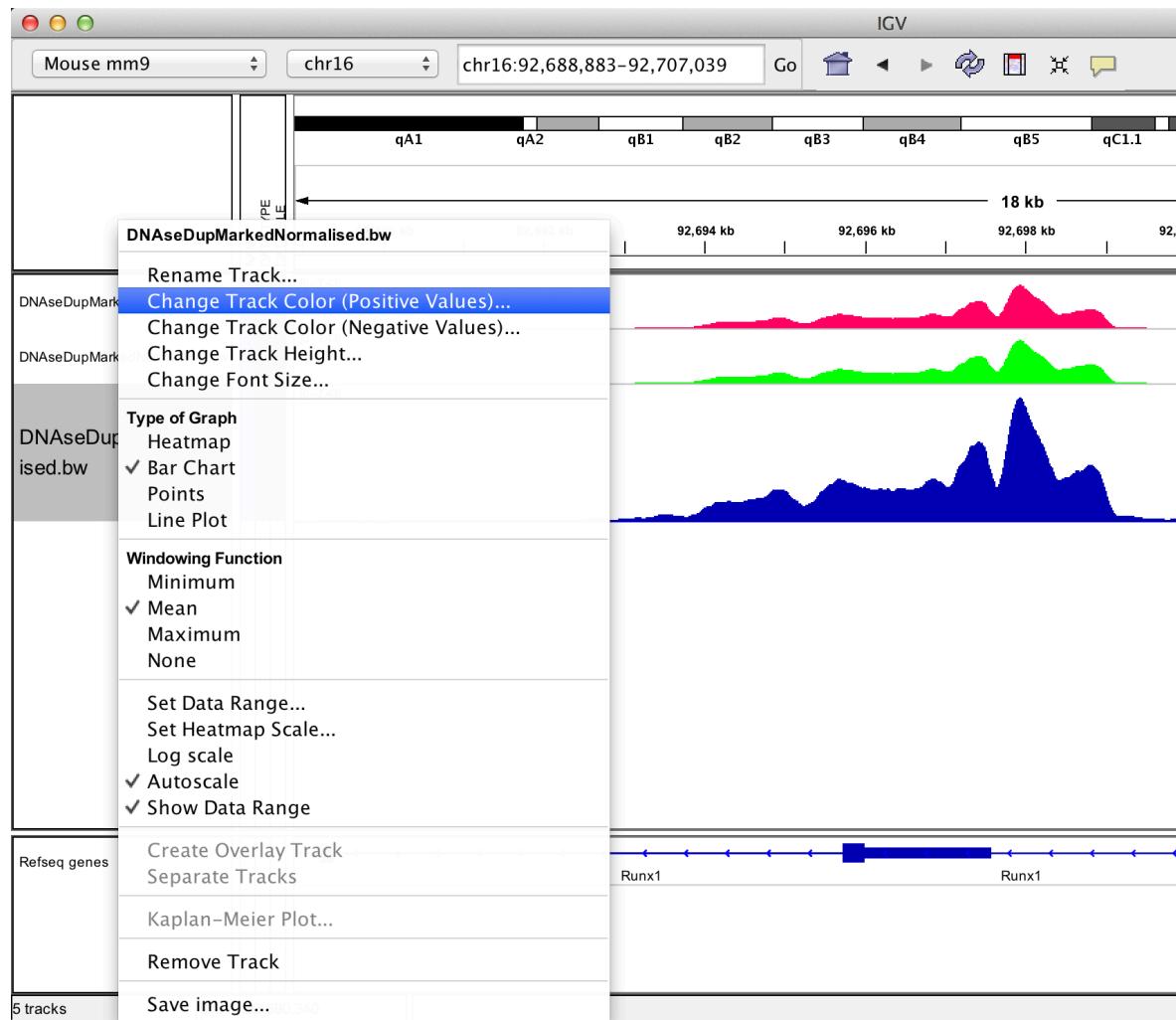
- Read Packing, grouping, sorting, colouring options.



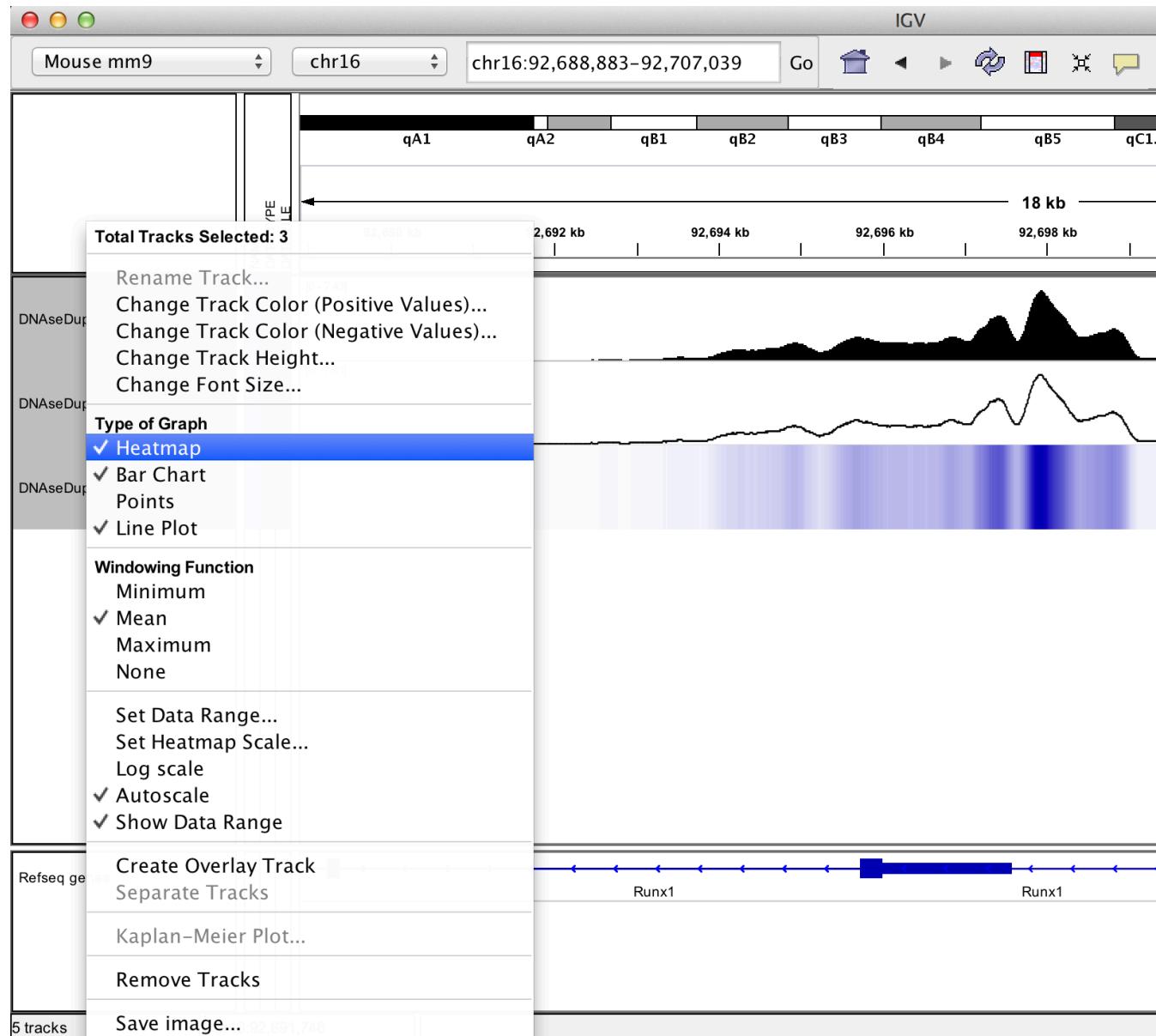
# Track display options

## Graph/interval files

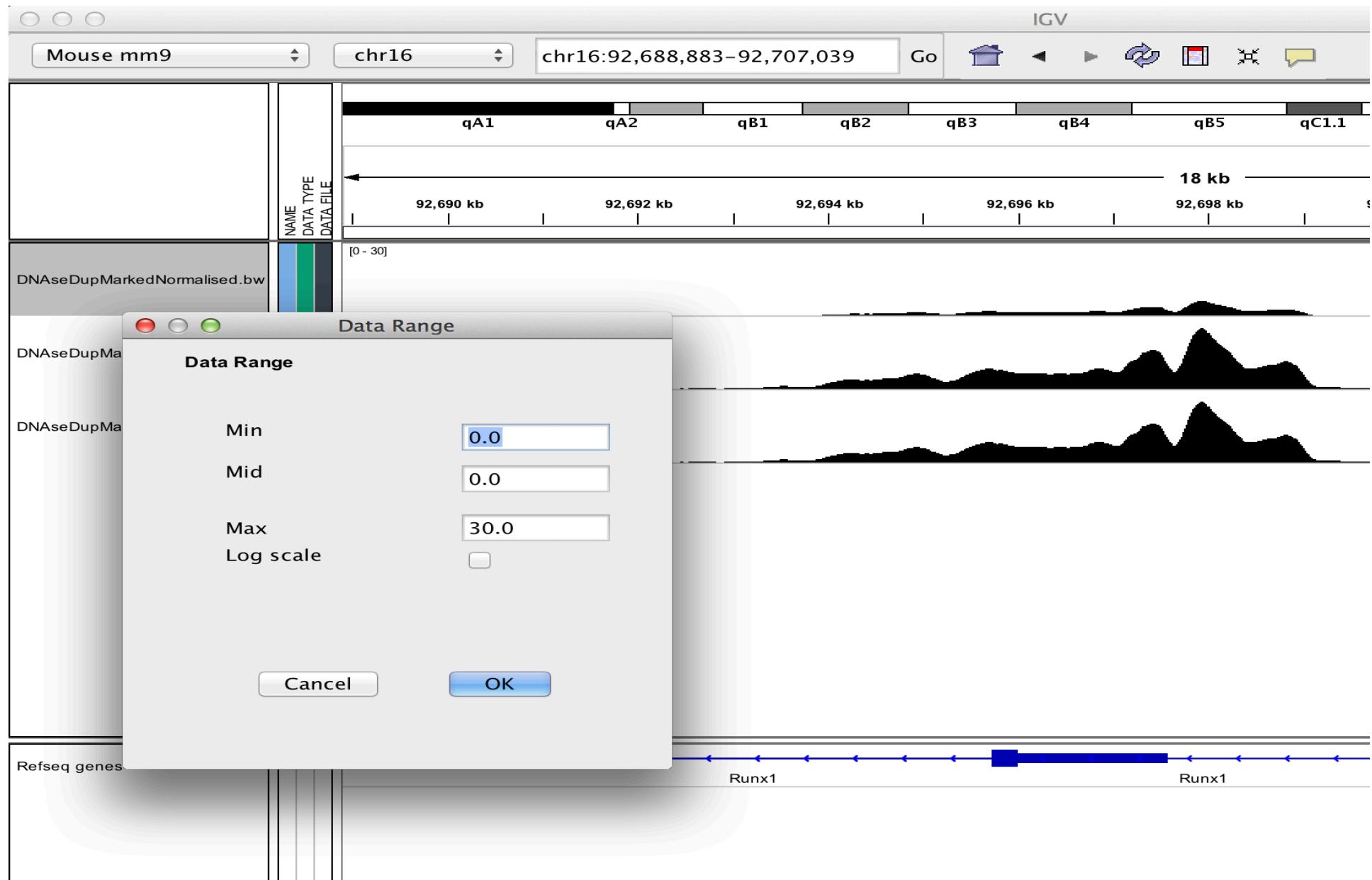
- Track colour/appearance



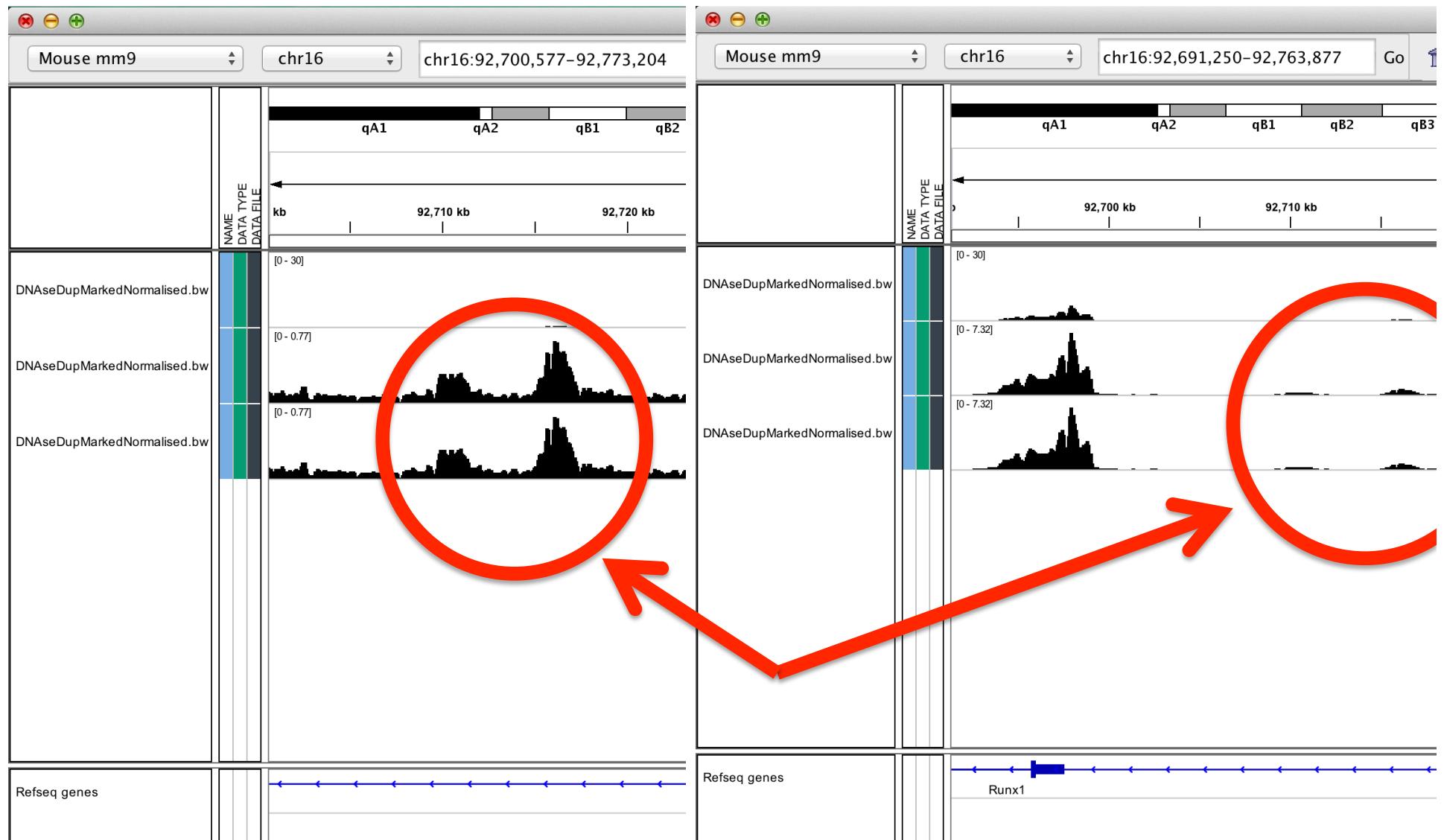
## ■ Graph type



# Data Scaling.

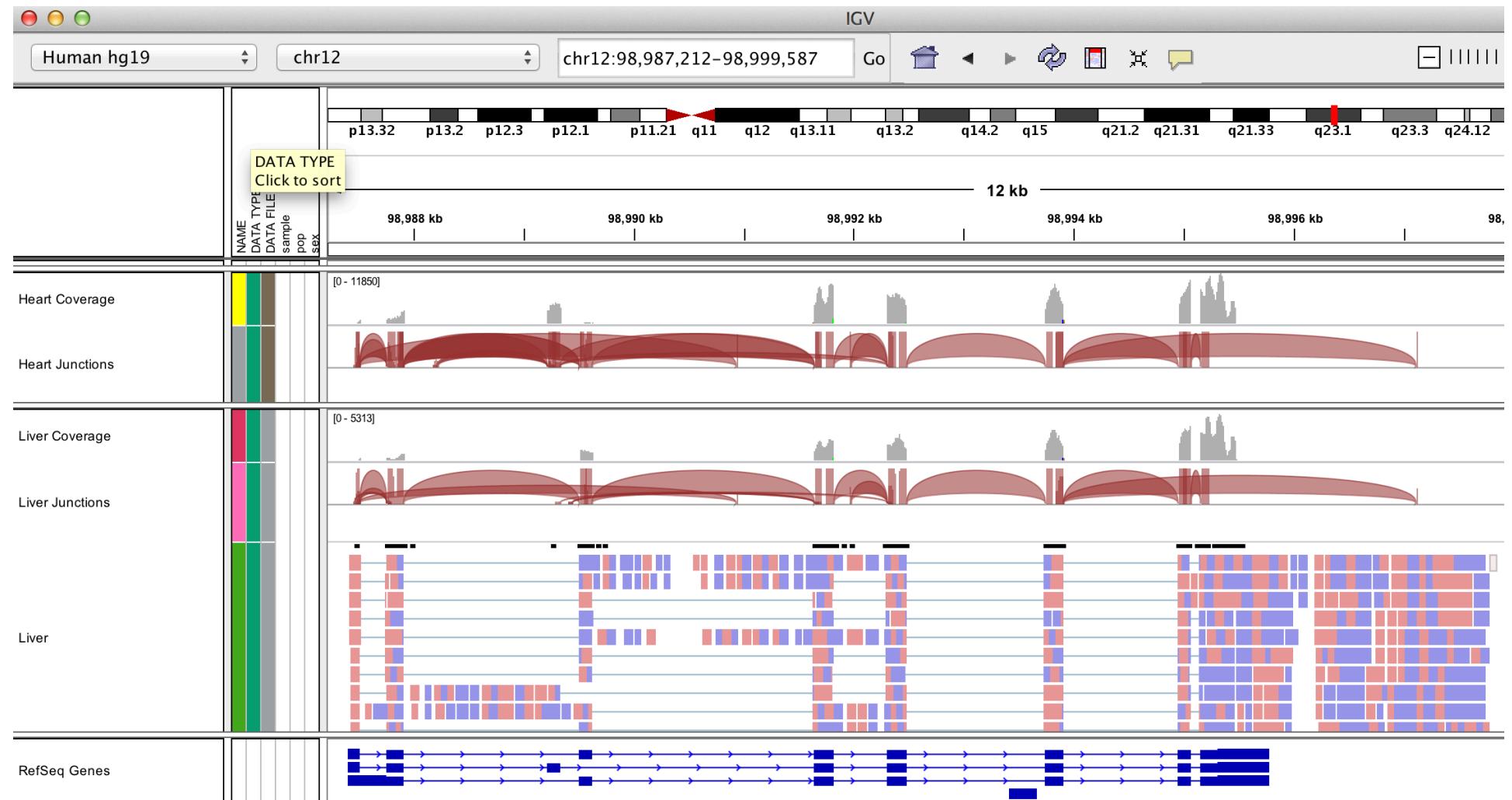


- Autoscaling adjusts to track's visible signal maximum



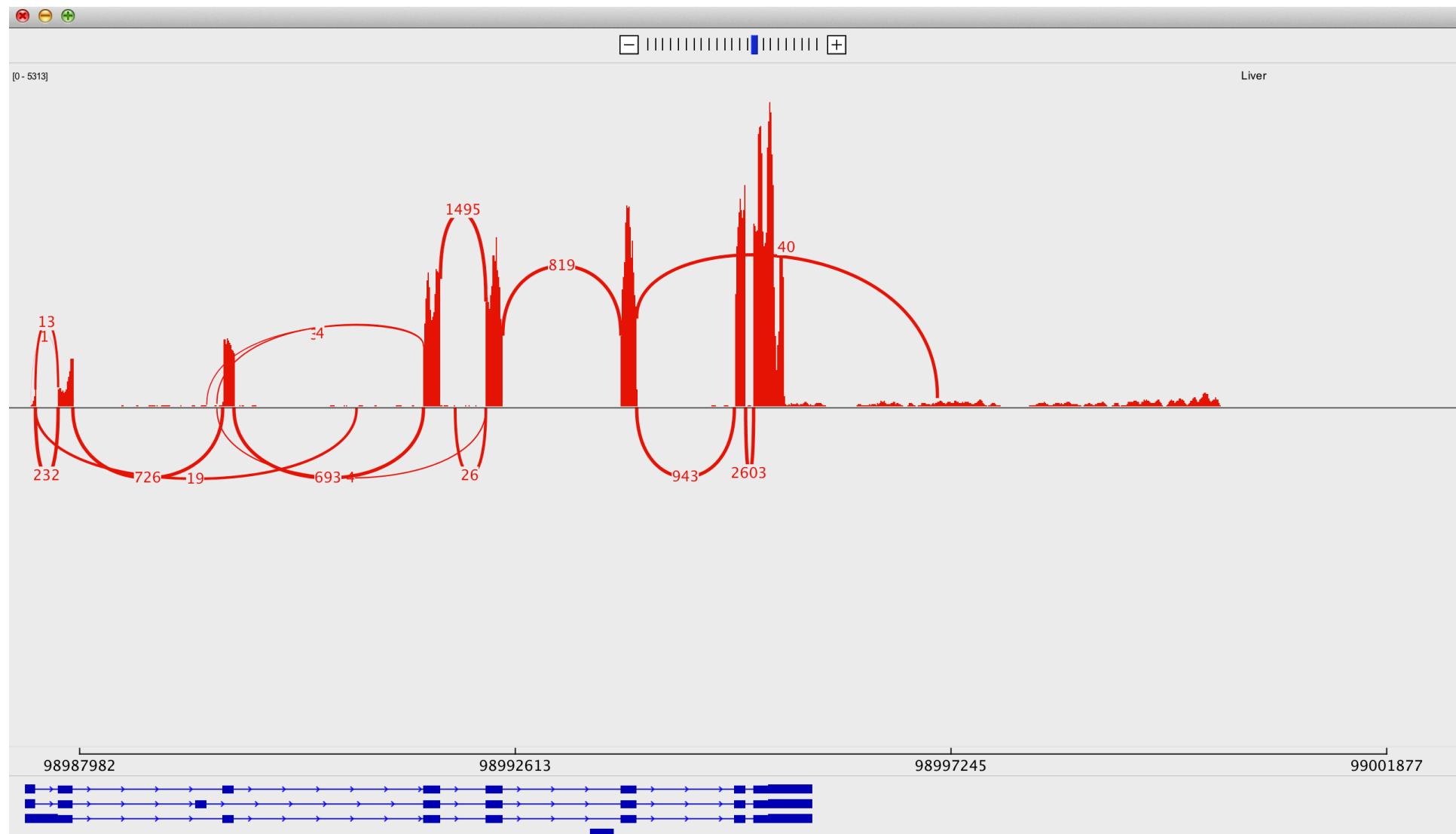
Some cool features.

# IGV can display splicing information

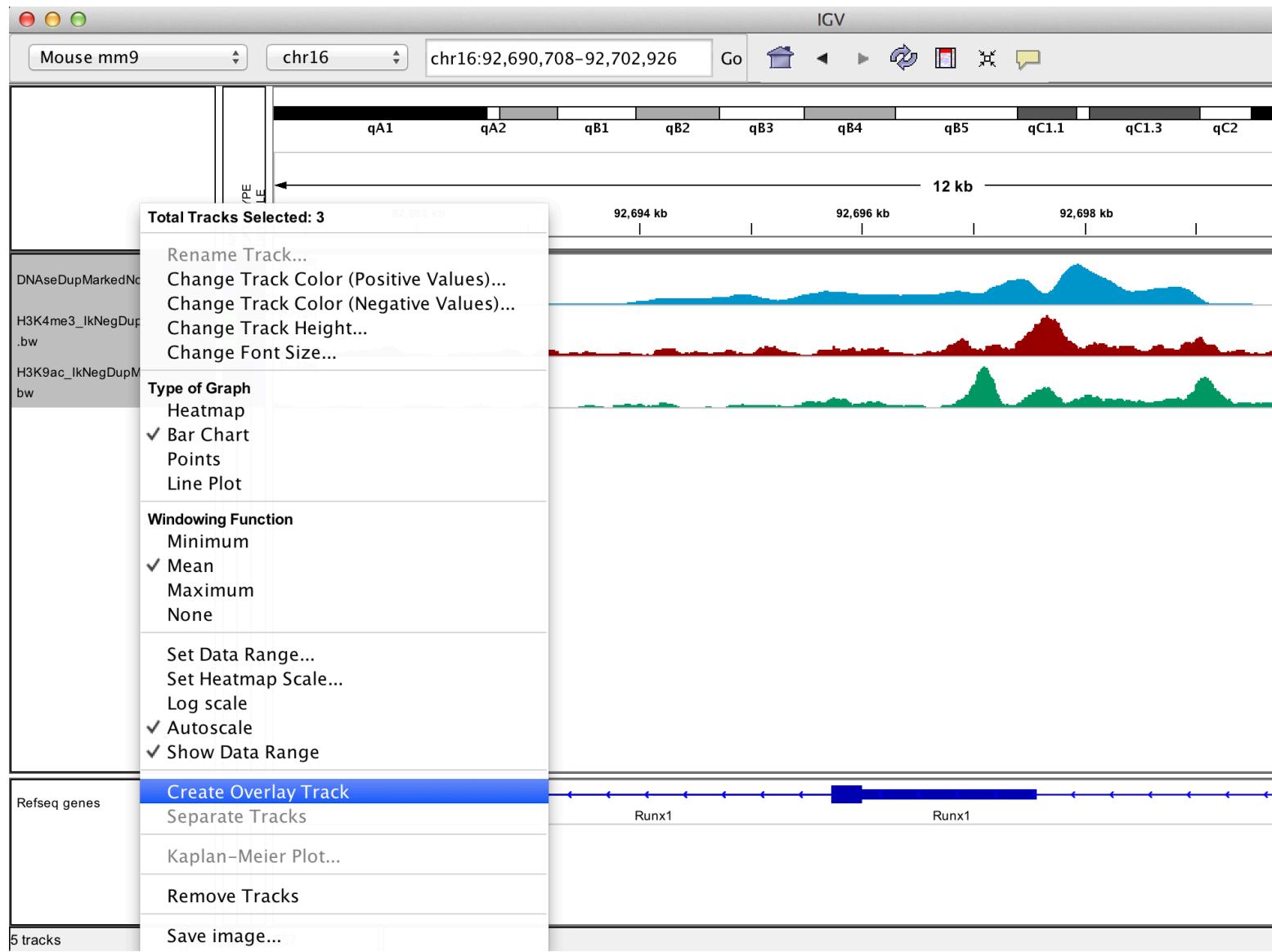


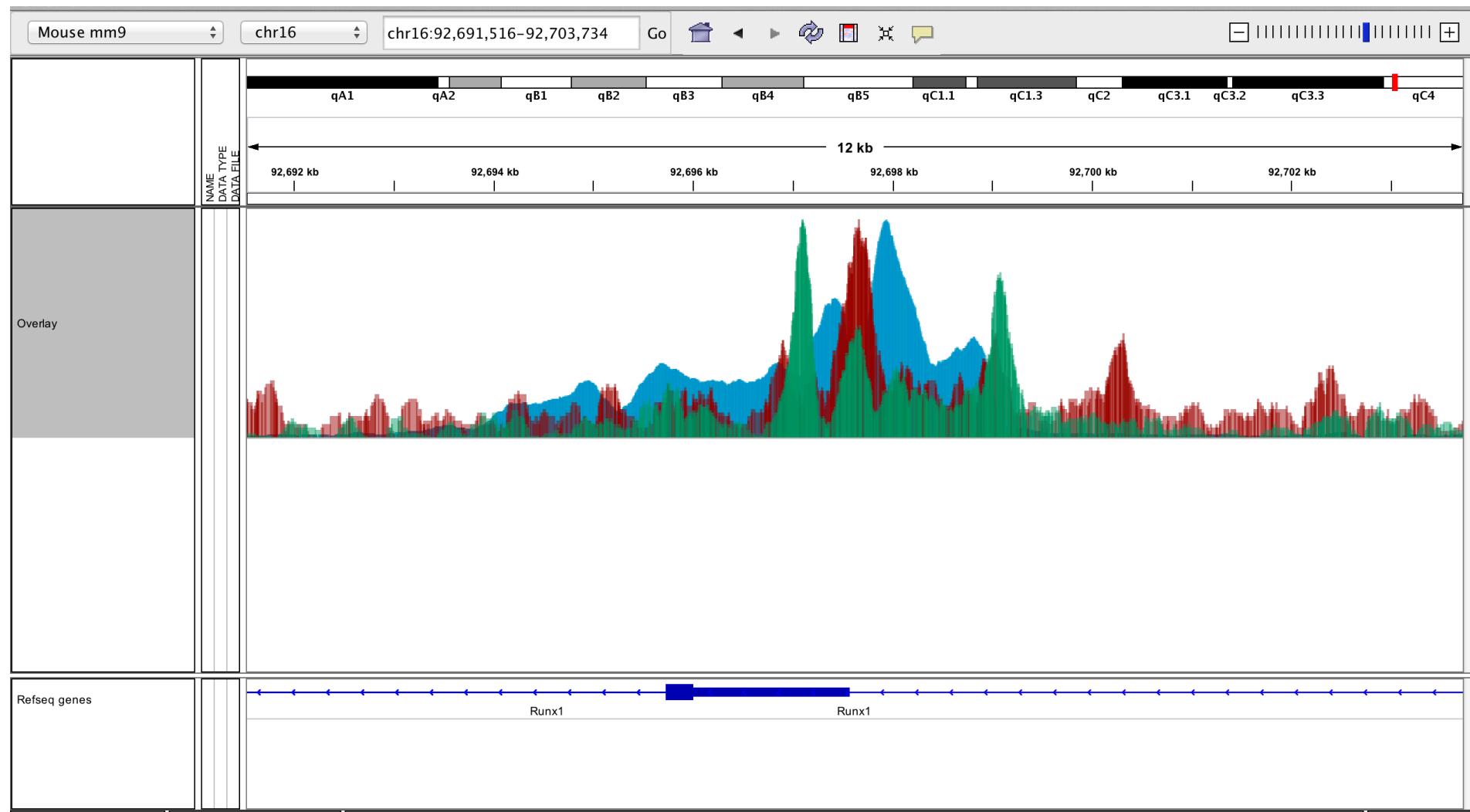
# ..and Sashimi plots

(<http://www.broadinstitute.org/igv/Sashimi>)



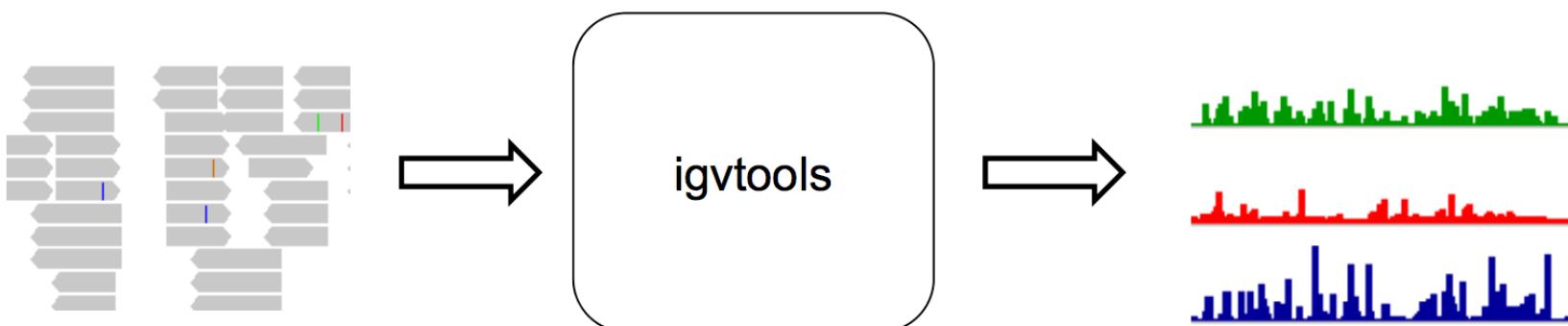
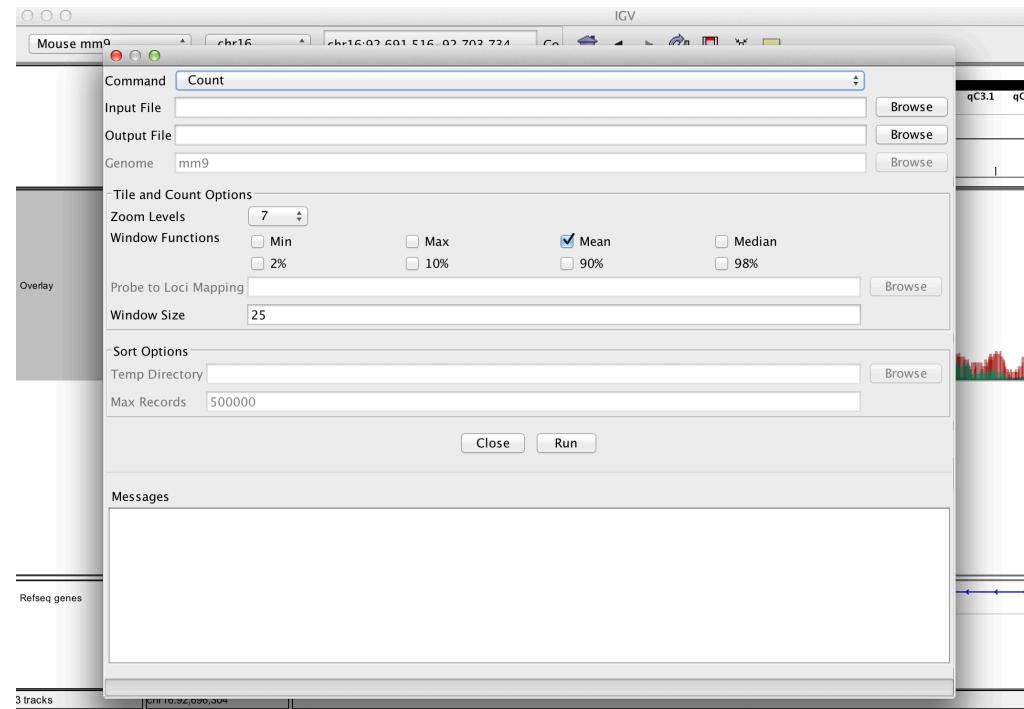
# IGV can overlay tracks too.





# IGV includes a simple toolset IGVTools

- IGVTools can be used to post-process genomics data.
- Includes indexing, sorting and genome graph creation.



# Where to get help?

- <http://www.broadinstitute.org/igv/UserGuide>
- <https://groups.google.com/forum/#!forum/igv-help>